

Cook, L.
09/16/2003
Seq. ID 1 w/in Page 1

GenCore version 4.5
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OM protein - protein search, using sw model.

Run on: June 6, 2002, 13:03:48 ; Search time 105.16 Seconds

(without alignments)
20.083 Million cell updates/sec

Title: US-09-627-383-1

Perfect score: 29

Sequence: 1 LEPRAS 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters:

3502263

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	29	100.0	6	20 US-09-627-383-1
2	29	100.0	67	26 US-09-627-383-1
3	29	100.0	75	1 PCT-US01-14827-12024
4	29	100.0	108	1 PCT-US01-14827-14753
5	29	100.0	119	1 PCT-US01-7642
6	29	100.0	153	21 US-09-378-472-5581
7	100.0	256	12	US-08-878-322-11

RESULT 1

US-09-627-383-1

; Sequence 1, Application US/09627383.

; GENERAL INFORMATION:

; APPLICANT: Paul T. Matsudaira

; APPLICANT: Daniel J. Ehrlich

; APPLICANT: QiuHui Zhang

; APPLICANT: Yelena Freyzen

; TITLE OF INVENTION: Affinity Fluorescent Proteins and Uses

; FILE REFERENCE: Thereof

; CURRENT APPLICATION NUMBER: US/09-627-383

; CURRENT FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/146,438

; PRIOR APPLICATION NUMBER: US 60/061,801

; PRIOR FILING DATE: 1997-10-14

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSEED for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Hexapeptide

; US-09-627-383-1

ALIGNMENTS

8	29	100.0	256	14 US-09-099-295-11	Sequence 11, Appl
9	29	100.0	256	22 US-09-852-477-11	Sequence 11, Appl
10	29	100.0	258	21 US-09-758-441-688	Sequence 11, Appl
11	29	100.0	421	23 US-09-902-540-13318	Sequence 13318, A
12	29	100.0	439	16 US-09-270-767-57034	Sequence 57034, A
13	29	100.0	439	16 US-09-270-849-180914	Sequence 406, App
14	29	100.0	471	26 US-60-206-047-406	Sequence 531, App
15	29	100.0	634	26 US-60-171-628-531	Sequence 5225, A
16	29	100.0	634	26 US-60-173-464-26180	Sequence 14791, A
17	29	100.0	635	20 US-09-614-150-34179	Sequence 3179, A
18	29	100.0	635	26 US-60-191-637-33763	Sequence 33763, A
19	29	100.0	635	26 US-60-191-681-22617	Sequence 26617, A
20	29	100.0	635	26 US-60-219-005-312	Sequence 312, App
21	29	100.0	637	1 PCT-US01-08631-52925	Sequence 1824, Ap
22	29	100.0	666	18 US-09-488-723A-1823	Sequence 1823, Ap
23	29	100.0	682	1 PCT-US00-25340-1	Sequence 7726, Ap
24	29	100.0	708	12 US-08-878-322-8	Sequence 1825, Ap
25	29	100.0	708	14 US-09-059-295-8	Sequence 6181, Ap
26	29	100.0	708	22 US-09-852-472-8	Sequence 10764, A
27	29	100.0	966	18 US-09-488-723A-1824	Sequence 10786, A
28	29	100.0	1013	18 US-09-488-723A-1823	Sequence 8743, Ap
29	29	100.0	1021	26 US-60-167-217-726	Sequence 25, App
30	29	100.0	1025	18 US-09-488-723A-1825	Sequence 1, Appl
31	29	100.0	1050	26 US-60-173-464-6181	Sequence 8465, Ap
32	29	100.0	1077	20 US-09-614-150-10764	Sequence 4, Appl
33	29	100.0	1077	26 US-60-167-210-10786	Sequence 2, Appl
34	29	100.0	1077	26 US-60-173-464-8743	Sequence 1, Appl
35	29	100.0	1077	26 US-60-191-637-10796	Sequence 10796, A
36	29	100.0	1077	26 PCT-US99-14482-4	Sequence 8465, Ap
37	29	100.0	1219	17 US-09-344-624-4	Sequence 4, Appl
38	29	100.0	1219	17 US-09-344-624-4	Sequence 2, Appl
39	29	100.0	1253	1 PCT-US99-19663-2	Sequence 1, Appl
40	29	100.0	1253	17 US-09-389-089-2	Sequence 2, Appl
41	29	100.0	2359	17 US-09-346-794-26	Sequence 26, Appl
42	29	100.0	2359	20 US-09-611-257-26	Sequence 1, Appl
43	29	100.0	2548	22 US-09-851-682-1	Sequence 1, Appl
44	29	100.0	2548	22 US-09-851-682-1	Sequence 2, Appl
45	29	100.0	2887	21 US-09-851-682-1	Sequence 1, Appl

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPRAS 6
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Db 1 LEPRAS 6

RESULT 2
US-60-146-315-866
; Sequence 866, Application US/60146315
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED KINASE PROTEINS, NUCLEIC ACID
; FILE REFERENCE: CLO00064
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIORITY NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SEQ ID NO 14753
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila
; US-60-146-315-866

Query Match 100.0%; Score 29; DB 26; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPRAS 6
    ||||| 6
Db 16 LEPRAS 21

RESULT 3
PCT-US01-14827-12024
; Sequence 12024, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEAR ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 2127-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 12024
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (30)..(41)
; OTHER INFORMATION: PROTEIN SPORULATION REPEAT PRECQ domain identified by
; OTHER INFORMATION: emATRIX, accession number PD02283B, p-value=7.857e-09, raw score
; OTHER INFORMATION: 8.67
; PCT-US01-14827-12024

Query Match 100.0%; Score 29; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPRAS 6
    ||||| 6
Db 63 LEPRAS 68

RESULT 4
PCT-US01-14827-14753
; Sequence 14753, Application PC/TUS0114827

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PRIOR FILING DATE: 2000-02-04
 NUMBER OF SEQ ID NOS: 9632
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 5581
 LENGTH: 153

ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (115)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (122)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (123)

Query Match 100.0%; Score 29; DB 21; Length 153;
 Best Local Similarity 100.0%; Pred. No. 8 5e+02; Mismatches 0;
 Matches 6; Conservative 0; Strandness 0;

US-09-758-472-5581

RESULT 8
 US-09-999-295-11
 Sequence 11, Application US/09099295
 GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.

APPLICANT:

Jelinek, Laura J.

APPLICANT:

Whitmore, Theodore E.

APPLICANT:

Blumberg, Hal

APPLICANT:

Leiner, Joyce M.

APPLICANT:

Mammalian Neuro-Growth Factor Like Protein

TITLE OF INVENTION: MAMMALIAN NEURO-GROWTH FACTOR LIKE PROTEIN

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc.

STREET: 1201 Eastlake Ave. East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/099,295

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G.

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 97-28

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 256 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-099-295-11

RESULT 7
 US-08-878-322-11
 Sequence 11, Application US/08878322
 GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.
 APPLICANT: Jelinek, Laura J.
 APPLICANT: Whitmore, Theodore E.

APPLICANT: Blumberg, Hal
 TITLE OF INVENTION: MAMMALIAN ZNEU1
 NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc.
 STREET: 1201 Eastlake Ave. East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/878,322

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G.

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 97-28

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 256 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-099-295-11

RESULT 9
 US-09-627-383-1.rapm
 Query Match 100.0%; Score 29; DB 14; Length 256;
 Best Local Similarity 100.0%; Pred. No. 8 5e+02; Mismatches 0;
 Matches 6; Conservative 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 Db 146 LEPRAS 151

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 256 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

ORIGINAL SOURCE:

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; Sequence 11; Application US/09852472
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Mammalian Neuro-Growth Factor Like
; FILE REFERENCE: 97-28C1
; CURRENT APPLICATION NUMBER: US/09/852,472
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/099,295
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/050,143
; PRIOR FILING DATE: 1997-06-18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-852-472-11

Query Match          100.0%; Score 29; DB 22; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEPRAS 6
Db      146 LEPRAS 151

RESULT 10
US-09-758-440-688
; Sequence 688, Application US/09758440
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic acids, Proteins, and Antibodies
; FILE REFERENCE: PM015
; CURRENT APPLICATION NUMBER: US/09/758,440
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,629
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 832
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 688
; LENGTH: 258
; TYPE: PRT
; FEATURE:
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-758-440-688

Query Match          100.0%; Score 29; DB 21; Length 258;
Best Local Similarity 100.0%; Pred. No. 8.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEPRAS 6
Db      146 LEPRAS 151

RESULT 11
US-09-902-540-13318
; Sequence 13318, Application US/09902540
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

Query Match          100.0%; Score 29; DB 23; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEPRAS 6
Db      406 LEPRAS 411

RESULT 12
US-09-270-767-57034
; Sequence 57034, Application US/09270767
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 57034
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-57034

Query Match          100.0%; Score 29; DB 16; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEPRAS 6
Db      196 LEPRAS 201

RESULT 13
US-09-270-849B-180914
; Sequence 180914, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 195450
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 180914
; LENGTH: 439
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: at any location having Xaa, Xaa means any amino acid
; US-09-270-849B-180914

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Query Match 100.0%; Score 29; DB 16; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03; Length 439;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 196 LEPRAS 201

RESULT 14

US-60-206-047-406
 Sequence 406, Application US/60206047

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen
 TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF

FILE REFERENCE: C1000570

CURRENT APPLICATION NUMBER: US/60/206, 047

CURRENT FILING DATE: 2000-05-22

NUMBER OF SEQ ID NOS: 456

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 406

LENGTH: 471

TYPE: PRT

ORGANISM: HUMAN

US-60-206-047-406

Query Match 100.0%; Score 29; DB 26; Length 471;

Best Local Similarity 100.0%; Pred. No. 1.7e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 282 LEPRAS 287

RESULT 15

US-60-171-625-531

Sequence 531, Application US/60171625

GENERAL INFORMATION:

APPLICANT: Skupski, Marian

TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS THAT SHOW HIGH HOMOLOGY TO KNOWN HUMAN DISEASE PROTEINS, AND USES THEREOF

FILE REFERENCE: C1000179

CURRENT APPLICATION NUMBER: US/60/171, 625

CURRENT FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 579

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO: 531

LENGTH: 634

TYPE: PRT

ORGANISM: DROSOPHILA

US-60-171-625-531

Query Match 100.0%; Score 29; DB 26; Length 634;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03; Length 634;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 26 LEPRAS 31

Search completed: June 6, 2002, 13:07:20
 Job time: 212 sec

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OM protein - protein search, using SW model.

Run on: June 6, 2002, 13:03:48 ; Search time 12.67 Seconds
(without alignments)
27.907 Million cell updates/sec

Title: US-09-627-383-1

Perfect score: 29

Sequence: 1 LEPRSS 6

Scoring table: BLOSUM62

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Searched: 186664 seqs, 5893091 residues

Total number of hits satisfying chosen parameters: 186664

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6_ptodata/_2/paa/US07_NEW_COMB.pep:*

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7: /cgn2_6_ptodata/_2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description		
1	26	89.7	61	5 US-09-540-209B-9237	Sequence 9237, APP		
2	26	89.7	153	6 US-10-121-062-564	Sequence 564, APP		
3	26	89.7	406	1 PCT-US02-11152-21	Sequence 21, APP		
4	26	89.7	485	1 PCT-US02-11152-20	Sequence 20, APP		
5	26	89.7	8360	6 US-10-132-134-34	Sequence 34, APP		
6	25	86.2	24	1 PCT-US02-07282-6	Sequence 6, APP		
7	25	86.2	24	6 US-10-114-500-6	Sequence 6, APP		
8	25	86.2	58	5 US-09-859-604-538	Sequence 538, APP		
9	25	86.2	177	6 US-10-113-872-1863	Sequence 1678, APP		
10	25	86.2	214	5 US-09-540-209B-5669	Sequence 569, APP		
11	25	86.2	241	5 US-09-935-625-23288	Sequence 23288, APP		
12	25	86.2	283	6 US-09-935-625-28	Sequence 28, APP		
13	25	86.2	287	5 US-09-935-625-23287	Sequence 23287, APP		
14	25	86.2	314	6 US-10-113-872-1863	Sequence 1863, APP		
15	25	86.2	357	7 US-60-377-714-52	Sequence 52, APP		
16	25	86.2	439	1 PCT-US02-07282-4	Sequence 4, APP		
17	25	86.2	439	6 US-10-114-500-4	Sequence 4, APP		
18	25	86.2	475	5 US-09-935-625-13383	Sequence 13383, APP		
19	25	86.2	475	5 US-09-935-625-21538	Sequence 21538, APP		
20	25	86.2	475	5 US-09-935-625-30024	Sequence 30024, APP		
21	25	86.2	535	5 US-09-935-625-13382	Sequence 13382, APP		
22	25	86.2	535	5 US-09-935-625-21537	Sequence 21537, APP		
23	25	86.2	535	5 US-09-935-625-30023	Sequence 30023, APP		
24	25	86.2	551	5 US-09-935-625-11615	Sequence 11615, APP		
25	25	86.2	551	5 US-09-935-625-19542	Sequence 19542, APP		
551	86.2			Sequence 28022, APP	Sequence 28022, APP		

RESULT 1

US-09-540-209B-9237

; Sequence 9237, Application US/09540209B

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton

; TITLE OF INVENTION: FORBIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709_1001-001

; CURRENT APPLICATION NUMBER: US/09/540, 209B

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 1044

; SEQ ID NO: 9237

; LENGTH: 61

; TYPE: PRT

; ORGANISM: B.fragilis

US-09-540-209B-9237

Query Match 89.7%; Score 26; DB 5; Length 61;

Best Local Similarity 83.3%; Pred. No. 29;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 LEPRSS 6

QY |||||

RESULT 2

US-10-121-062-564

; Sequence 564, Application US/10121062

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Destroyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godkowsky, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanaabe, Collin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhenin, Zhang

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C1

; CURRENT APPLICATION NUMBER: US/10/121, 062

; CURRENT FILING DATE: 2002-04-12

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO: 564	Query Match	89.7%	Score 26;	DB 1;	Length 406;
LENGTH: 153	Best Local Similarity	83.3%	Pred. No. 2.3e+02;		
TYPE: PRT	Matches	5;	Conservative	1;	Mismatches 0;
ORGANISM: Homo Sapien	Indels	0;	Gaps	0;	
US-10-121-062-564	Qy	1 LEPRSS 6	Db	145 LEPRSS 150	
RESULT 3	PCT-US02-11152-21	Sequence 21, Application PC/TUS0211152	RESULT 4	PCT-US02-11152-20	Sequence 20, Application PC/TUS0211152
GENERAL INFORMATION:					
APPLICANT: INCYTE GENOMICS, INC.					
APPLICANT: AZIMZAI, Yalda					
APPLICANT: AU-YOUNG, Janice K.					
APPLICANT: BATRA, Sajeer					
APPLICANT: BAUGHN, Mariah R.					
APPLICANT: BECHA, Shanya D.					
APPLICANT: BOROWSKY, Mark L.					
APPLICANT: BUFORD, Neil					
APPLICANT: DING, Li					
APPLICANT: ELLIOTT, Vicki S.					
APPLICANT: EMERLING, Brooke M.					
APPLICANT: GANDHI, Amneena R.					
APPLICANT: GIETZEN, Kimberly J.					
APPLICANT: GRIFFIN, Jennifer A.					
APPLICANT: HAFALIA, April J.A.					
APPLICANT: HONCHELL, Cynthia D.					
APPLICANT: LAL, Preeti G.					
APPLICANT: LEE, Soo Yeun					
APPLICANT: LU, Dzung Aina M.					
APPLICANT: ARVIZU, Chandra S.					
APPLICANT: RAMKUMAR, Jayalakshmi					
APPLICANT: REDDY, Roopa					
APPLICANT: SANJANWALA, Madhu, M.					
APPLICANT: TANG, Y. Tom					
APPLICANT: WALIA, Narinder K.					
APPLICANT: WANG, Yu-mei, E.					
APPLICANT: WARREN, Bridget A.					
APPLICANT: XU, Yunling					
APPLICANT: YANG, Junming					
APPLICANT: YAO, Monique G.					
APPLICANT: YUE, Henry					
APPLICANT: ZEBARAJDAN, Yeganeh					
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH	TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH	TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH	TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH	TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH	TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PI-0417.PCT					
CURRENT APPLICATION NUMBER: PCT/US02/11152					
CURRENT FILING DATE: 2002-04-05					
PRIOR APPLICATION NUMBER: 60/282,110; 60/283,294; 60/286,820; 60/287,228;					
60/291,662; 60/291,846; 60/293,727; 60/295,340;	60/291,662; 60/291,846; 60/293,727; 60/295,340;	60/291,662; 60/291,846; 60/293,727; 60/295,340;	60/291,662; 60/291,846; 60/293,727; 60/295,340;	60/291,662; 60/291,846; 60/293,727; 60/295,340;	60/291,662; 60/291,846; 60/293,727; 60/295,340;
60/295,263; 60/349,705	60/295,263; 60/349,705	60/295,263; 60/349,705	60/295,263; 60/349,705	60/295,263; 60/349,705	60/295,263; 60/349,705
PRIOR FILING DATE: 2001-04-05; 2001-04-11; 2001-04-25; 2001-04-27;					
2001-05-16; 2001-05-18; 2001-05-25; 2001-06-01;	2001-05-16; 2001-05-18; 2001-05-25; 2001-06-01;	2001-05-16; 2001-05-18; 2001-05-25; 2001-06-01;	2001-05-16; 2001-05-18; 2001-05-25; 2001-06-01;	2001-05-16; 2001-05-18; 2001-05-25; 2001-06-01;	2001-05-16; 2001-05-18; 2001-05-25; 2001-06-01;
2001-06-01; 2002-01-15	2001-06-01; 2002-01-15	2001-06-01; 2002-01-15	2001-06-01; 2002-01-15	2001-06-01; 2002-01-15	2001-06-01; 2002-01-15
NUMBER OF SEQ ID NOS: 42					
SOFTWARE: PERL Program					
SEQ ID NO: 21	SEQ ID NO: 21	SEQ ID NO: 20			
LENGTH: 406	LENGTH: 406	LENGTH: 485	LENGTH: 485	LENGTH: 485	LENGTH: 485
TYPE: PRT					
ORGANISM: Homo sapiens					
FEATURE:	FEATURE:	FEATURE:	FEATURE:	FEATURE:	FEATURE:
NAME/KEY: misc_feature					
OTHER INFORMATION: Incyte ID No: 7506195CD1	OTHER INFORMATION: Incyte ID No: 7506195CD1	OTHER INFORMATION: Incyte ID No: 4558650CD1			
PCT-US02-11152-21	PCT-US02-11152-20	PCT-US02-11152-20	PCT-US02-11152-20	PCT-US02-11152-20	PCT-US02-11152-20

```

Db 62 LQPRAS 67
| :|||||
RESULT 5
US-10-132-134-34
; Sequence 34, Application US/10132134
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Yang, Xianshu
; APPLICANT: Staffa, Alfredo
; APPLICANT: Zazopoulos, Emmanuel
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES
; FILE REFERENCE: 3012-2US
; CURRENT APPLICATION NUMBER: US/10/132,134
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 8360
; TYPE: PRT
; ORGANISM: Streptomyces amphibiosporus
; US-10-132-134-34

Query Match 86.2%; Score 25; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPRAS 6
|||:|
Db 6398 LEPRAS 6403

*RESULT 6
PCT-US02-07282-6
Sequence 6, Application PC/TUS0207/282
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Boyle, Bryan J
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Liu, Chenghua
; APPLICANT: Tang, Y Tom
; APPLICANT: Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: POLYNUCLEOTIDES
; FILE REFERENCE: 24059-000-061
; CURRENT APPLICATION NUMBER: PCT/US02/07282
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/802,704
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-132-134-34

Query Match 89.7%; Score 26; DB 6; Length 8360;
Best Local Similarity 83.3%; Pred. No. 5.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPRAS 6
|||:|
Db 6398 LEPRAS 6403

*RESULT 6
PCT-US02-07282-6
Sequence 6, Application PC/TUS0207/282
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Boyle, Bryan J
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Liu, Chenghua
; APPLICANT: Tang, Y Tom
; APPLICANT: Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: POLYNUCLEOTIDES
; FILE REFERENCE: 24059-000-061
; CURRENT APPLICATION NUMBER: PCT/US02/07282
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 09/802,704
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-132-134-34

Query Match 86.2%; Score 25; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EPRAS 6
|||:|
Db 20 EPRAS 24

*RESULT 8
US-09-855-604-538
Sequence 538, Application US/09855604
; GENERAL INFORMATION:
; APPLICANT: Gicodel, Brigitte
; APPLICANT: Poronoi, Denis
; APPLICANT: Lim, Eng-Mong
; APPLICANT: Pellicic, Vladimir
; APPLICANT: Gutuено, Agnes
; APPLICANT: Goget, De La Salmoniere, Yves
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0052-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-06-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; US-09-855-604-538

Query Match 86.2%; Score 25; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EPRAS 6
|||:|
Db 20 EPRAS 24

```

Query Match Similarity 86.2%; Score 25; DB 5; Length 58;
 Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2 EPRAS 6	Db	4 EPRAS 8

RESULT 9
 US-10-113-872-1678
 ; Sequence 1678, Application US/10113872
 ; GENERAL INFORMATION:
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Barrick
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121-478C19
 ; CURRENT APPLICATION NUMBER: US/10/113,872
 ; CURRENT FILING DATE: 2002-03-28
 ; NUMBER OF SEQ ID NOS: 2011
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1678
 ; LENGTH: 177
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-113-872-1678

Query Match Similarity 86.2%; Score 25; DB 6; Length 177;
 Best Local Similarity 100.0%; Pred. No. 1.6e-02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2 EPRAS 6	Db	20 EPRAS 24

RESULT 10
 US-09-540-209B-5669
 ; Sequence 5669, Application US/09540209B
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRP
 ; FILE REFERENCE: 2709-1001-001
 ; CURRENT APPLICATION NUMBER: US/09/540, 209B
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 10444
 ; SEQ ID NO 5669
 ; LENGTH: 214
 ; TYPE: PRT
 ; ORGANISM: B fragilis
 ; US-09-540-209B-5669

Query Match Similarity 86.2%; Score 25; DB 5; Length 214;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;

Qy	1 LEPPRA 5	Db	4 LEPPRA 8

RESULT 11
 US-09-935-625-23288
 ; Sequence 23288, Application US/09935625

Query Match Similarity 86.2%; Score 25; DB 5; Length 58;
 Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 LEPPRA 5	Db	97 LEPPRA 101

RESULT 12
 US-09-895-913A-28
 ; Sequence 28, Application US/09895913A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kleanthou, Harold
 ; APPLICANT: Al-Garawi, Amal
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Tomb, Jean Francois
 ; APPLICANT: Omen, Raymond P.
 ; TITLE OF INVENTION: Identification of Polynucleotides
 ; TITLE OF INVENTION: Encoding Novel Helicobacter Polypeptides in the Helicobacter
 ; TITLE OF INVENTION: Genome
 ; FILE REFERENCE: 06132/043002
 ; CURRENT APPLICATION NUMBER: US/09/895, 913A
 ; CURRENT FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: US 08/881, 227
 ; PRIOR FILING DATE: 1997-06-24
 ; NUMBER OF SEQ ID NOS: 368
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 28
 ; LENGTH: 283
 ; TYPE: PRT
 ; ORGANISM: Helicobacter pylori
 ; US-09-895-913A-28

Query Match Similarity 86.2%; Score 25; DB 5; Length 283;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;

Qy	1 LEPPRA 5	Db	140 LEPPRA 144

RESULT 13
 US-09-935-625-23287
 ; Sequence 23287, Application US/09935625
 ; GENERAL INFORMATION:
 ; APPLICANT: N. ALEXANDROV et al.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
 ; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
 ; FILE REFERENCE: 2750-1481P
 ; CURRENT APPLICATION NUMBER: US/09/935, 625
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 33135
 ; SEQ ID NO 23288
 ; LENGTH: 241
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: peptide
 ; LOCATION: I..241
 ; OTHER INFORMATION: Ceres Seq. ID no. 2028609
 ; US-09-935-625-23288

NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 23287
LENGTH: 287
TYPE: PRY
ORGANISM: Arabidopsis thaliana
FEATURE: peptide
NAME/KEY: peptide
LOCATION: 1..287
OTHER INFORMATION: Ceres Seq. ID no. 2028608
US-09-935-625-23287

Query Match 86.2%; Score 25; DB 5; Length 287;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 LEPRA 5
Db 123 LEPRA 127

RESULT 14

US-10-113-872-1863

; Sequence 1863, Application US/10113872

GENERAL INFORMATION:

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Sleath, Paul R.

APPLICANT: Vedick, Thomas S.

APPLICANT: Carter, Derrick

APPLICANT: Ranger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.478C19

CURRENT FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 2011

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1863

LENGTH: 314

TYPE: PRY

ORGANISM: Homo sapiens

US-10-113-872-1863

Query Match 86.2%; Score 25; DB 7; Length 367;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 LEPRA 5
Db 132 LEPRA 136

Search completed: June 6, 2002, 13:04:51
Job time: 63 sec

RESULT 15

US-60-377-714-52

; Sequence 52, Application US/6037714

GENERAL INFORMATION:

APPLICANT: Ward, Teresa R

APPLICANT: Mao, Mao

APPLICANT: Linsley, Peter S

FILE REFERENCE: R02-016-200

CURRENT APPLICATION NUMBER: US/60/377,714

CURRENT FILING DATE: 2002-03-03

NUMBER OF SEQ ID NOS: 111

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 52

LENGTH: 367

TYPE: PRY

ORGANISM: Homo sapiens

US-60-377-714-52

Thu Jun 6 15:17:16 2002

us-09-627-383-1.rapn

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp wipo.int/pub/published_pot_sequences.

XX Sequence 125 AA;

	Query Match	Best Local Similarity	Score	DB	Length
Qy	1 LEPFRAS 6	100.0%	29;	22;	125;
Db	AAW8386 lepras 90	100.0%	Pred. No. 92;	Mismatches 0;	Indels 0;
AC	AAW8386;	0;	Gaps 0;		
DR	26-APR-1999 (first entry)				
XX	Mammalian Zneul polypeptide.				
DE					
XX					
KW	zneu-1; neuro-growth factor-like protein; human; breast cancer;				
KW	glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;				
KW	nerve regeneration; haemopoiesis; fertility; contraception;				
XX	antibody.				
OS	Class - Mammalia.				
PN	W09857983-A2.				
XX	PD 23-DEC-1998.				
PP	18-JUN-1998; 98WO-US12763.				
PR	18-JUN-1997; 97US-0878322.				
PR	18-JUN-1997; 97US-0050143.				
PA	(ZYMO) ZYMOGENETICS INC.				
XX	Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO;				
PI	Whitmore TE;				
XX	WPI; 1999-095324/08.				
PT	New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's				
PT	disease, cancer and to repopulate blood cells				
XX	PS Claim 6; Page 54; 70pp; English.				
DR	This polypeptide comprises a novel mammalian Zneul polypeptide.				
XX	Novel human Zneul (see AAW8381) is a new neuro-growth factor-like				
CC	protein that shows homology to Notch 4 and which may be involved in				
CC	EGF receptor pathways. Zneul can be used as a growth, maintenance,				
CC	or differentiation factor in the spinal cord, heart, spleen,				
CC	testis, thyroid and lymph nodes. It may also be used to treat				
CC	Alzheimer's disease, cancer, to repopulate blood cells after				
CC	chemotherapy, to stimulate myoblast proliferation, stimulate				
CC	or inhibit growth factors made in the placenta, in fertility and				
CC	contraction, or to regenerate nerves. Claimed Zneul polypeptides				
CC	(see also AAW8382-97), including specific domains of Zneul and				
CC	epitope bearing portions of Zneul, can be used to raise specific				
CC	antibodies for use e.g. in diagnostic assays.				
XX	Sequence 256 AA;				

	Matches	Conservative	Mismatches	Indels	Gaps
Qy	1 LEPFRAS 6	6	0;	0;	0;
ID	AAB93466 standard; Protein; 526 AA.	5			
XX	AAB93466;				
AC	AAB93466;				
XX	26-JUN-2001 (first entry)				
DE	Human protein sequence SEQ ID NO:12736.				
XX	Human; primer; detection; diagnosis; antisense therapy; gene therapy.				
XX	Homo sapiens.				
OS					
PN	EP1074617-A2.				
XX	PD 07-FEB-2001.				
XX	PF 28-JUL-2000; 2000EP-0116126.				
XX	PR 29-JUL-1999; 99JP-0248036.				
PR	27-AUG-1999; 99JP-0300253.				
PR	11-JAN-2000; 2000EP-0118776.				
PR	02-MAY-2000; 2000JP-0183767.				
PR	09-JUN-2000; 2000JP-0241899.				
PA	(HELI-) HELIX RES INST.				
XX	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;				
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;				
XX	WPI; 2001-318749/34.				
XX	Primer sets for synthesizing polynucleotides, particularly the 5602				
PT	and/or diagnosis of the abnormality of the proteins encoded by the				
PT	full-length cDNAs -				
PT	full-length cDNAs defined in the specification, and for the detection				
PT	of an oligonucleotide comprising a sequence complementary to the				
PT	full-length cDNAs defined in the specification. Where a primer set				
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary				
CC	to the complementary strand of a polynucleotide which comprises one of				
CC	the 5602 nucleotide sequences defined in the specification, where the				
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination				
CC	of an oligonucleotide comprising a sequence complementary to the				
CC	complementary strand of a polynucleotide which comprises a 5'-end				
CC	sequence and an oligonucleotide comprising a sequence complementary to a				
CC	polynucleotide which comprises a 3'-end sequence, where the				
CC	oligonucleotide comprises at least 15 nucleotides and the combination of				
CC	the 5'-end sequence/3'-end sequence is selected from those defined in				
CC	the specification. The primer sets can be used in antisense therapy and				
CC	in gene therapy. The primers are useful for synthesising polynucleotides,				
CC	particularly full-length cDNAs. The primers are also useful for the				
CC	detection and/or diagnosis of the abnormality of the proteins encoded by				
CC	the full-length cDNAs. The primers allow obtaining of the full-length				
CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and				
CC	AAH13633 to AAH1842 represent human cDNA sequences; AAB2446 to				
CC	AAB5893 represent human amino acid sequences; and AAH13629 to AAH13632				
CC	represent oligonucleotides, all of which are used in the exemplification				
XX	of the present invention.				

	Matches	Conservative	Mismatches	Indels	Gaps
Qy	1 LEPFRAS 6	6	0;	0;	0;
ID	AAB93466 standard; Protein; 526 AA.	5			
XX	AAB93466;				
AC	AAB93466;				
XX	26-JUN-2001 (first entry)				
DE	Human protein sequence SEQ ID NO:12736.				
XX	Human; primer; detection; diagnosis; antisense therapy; gene therapy.				
XX	Homo sapiens.				
OS					
PN	EP1074617-A2.				
XX	PD 07-FEB-2001.				
XX	PF 28-JUL-2000; 2000EP-0116126.				
XX	PR 29-JUL-1999; 99JP-0248036.				
PR	27-AUG-1999; 99JP-0300253.				
PR	11-JAN-2000; 2000EP-0118776.				
PR	02-MAY-2000; 2000JP-0183767.				
PR	09-JUN-2000; 2000JP-0241899.				
PA	(HELI-) HELIX RES INST.				
XX	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;				
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;				
XX	WPI; 2001-318749/34.				
XX	Primer sets for synthesizing polynucleotides, particularly the 5602				
PT	and/or diagnosis of the abnormality of the proteins encoded by the				
PT	full-length cDNAs -				
PT	full-length cDNAs defined in the specification, and for the detection				
PT	of an oligonucleotide comprising a sequence complementary to the				
PT	full-length cDNAs defined in the specification. Where a primer set				
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary				
CC	to the complementary strand of a polynucleotide which comprises one of				
CC	the 5602 nucleotide sequences defined in the specification, where the				
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination				
CC	of an oligonucleotide comprising a sequence complementary to the				
CC	complementary strand of a polynucleotide which comprises a 5'-end				
CC	sequence and an oligonucleotide comprising a sequence complementary to a				
CC	polynucleotide which comprises a 3'-end sequence, where the				
CC	oligonucleotide comprises at least 15 nucleotides and the combination of				
CC	the 5'-end sequence/3'-end sequence is selected from those defined in				
CC	the specification. The primer sets can be used in antisense therapy and				
CC	in gene therapy. The primers are useful for synthesising polynucleotides,				
CC	particularly full-length cDNAs. The primers are also useful for the				
CC	detection and/or diagnosis of the abnormality of the proteins encoded by				
CC	the full-length cDNAs. The primers allow obtaining of the full-length				
CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and				
CC	AAH13633 to AAH1842 represent human cDNA sequences; AAB2446 to				
CC	AAB5893 represent human amino acid sequences; and AAH13629 to AAH13632				
CC	represent oligonucleotides, all of which are used in the exemplification				
XX	of the present invention.				

Query Match 100.0%; Score 29; DB 20; Length 256;

Best Local Similarity 100.0%; Pred. No. 1.9e+02; Sequence 256 AA;

Query Match 100.0%; Score 29; DB 22; Length 526;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 |||||
 Db 335 lepras 340

RESULT 6

ABB69129 ABB69129 standard; Protein; 635 AA.
 ID XX
 AC XX
 XX
 DE DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 34179.
 KW XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 OS XX Drosophila melanogaster.
 OS XX WO200171042-A2.
 PN XX DR 27-SEP-2001.
 PD XX PR 23-MAR-2001; 2001WO-US09231.
 PR XX PE (PEKE) PE CORP NY.
 PA XX Venter JC, Adams M, Li PWD, Myers EW;
 PT XX WPI; 2001-658660/75.
 DR XX N-PSDB; ABL1232.

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 XX Disclosure; SEQ ID NO 34179; 21pp + Sequence Listing; English.

PT The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of diagnostics, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (AB57731-ABY2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 635 AA;

Query Match 100.0%; Score 29; DB 22; Length 635;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 |||||
 Db 27 lepras 32

RESULT 7

ABB22566 ABG32566 standard; Protein; 637 AA.
 ID XX

Query Match 100.0%; Score 29; DB 22; Length 637;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 |||||
 Db 202 lepras 207

RESULT 8

AAW88383 AAW88383 standard; Protein; 708 AA.
 ID XX

AC AAW88383;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE Mammalian Zneul polypeptide.
 XX
 KW Zneul-1; neuro-growth factor-like protein; human; breast cancer; glioblastoma; pituitary adenoma; Alzheimer's disease; therapy; nerve regeneration; haematopoiesis; fertility; contraception; antibody.
 KW
 OS Class - Mammalia.
 XX
 PN WO9857983-A2.
 XX
 PD 23-DEC-1998.
 XX
 PR 18-JUN-1998; 98WO-US12763.
 XX
 PR 18-JUN-1997; 97US-0878322.
 PR 18-JUN-1997; 97US-0050143.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO;
 PI Whitmore TE;
 XX
 DR WPI; 1999-095324/08.
 XX
 PT New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's disease, cancer and to repopulate blood cells
 XX
 Claim 6; Page 51-53; 70PP; English.
 PS
 XX
 EC This polypeptide comprises a novel mammalian Zneul polypeptide. Novel human Zneul (see AAW88381) is a new neuro-growth factor-like protein that shows homology to Notch 4 and which may be involved in EGR receptor pathways. Zneul can be used as a growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, thyroid and lymph nodes. It may also be used to treat Alzheimer's disease, cancer, to repopulate blood cells after chemotherapy, to stimulate myoblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and conception, or to regenerate nerves. Claimed Zneul polypeptides (see also AAW88382-97), including specific domains of Zneul and epitope-bearing portions of Zneul, can be used to raise specific antibodies for use e.g. in diagnostic assays.
 XX
 SQ Sequence 708 AA;

Query Match 100.0%; Score 29; DB 20; length 708;
 Best Local Similarity 100.0%; Pred. No. 5.1e-02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 ID AAM38679 standard; Protein; 966 AA.
 XX
 AC AAM38679;
 XX
 DT 22-OCT-2001 (first entry)

Human polypeptide SEQ ID NO 1824.

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
 KW
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0623450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J; Zhao QA, Zhou P, Goodrich R, Drmanac RR;
 XX
 DR WPI; 2001-442253/47.
 XX
 DR N-PSDB; AAI57835.
 PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
 XX
 PS Example 3; SEQ ID NO 1824; 10078PP; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM4213), with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed specification.
 XX
 SQ Sequence 966 AA;

Query Match 100.0%; Score 29; DB 22; length 966;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 ID AAM38678 standard; Protein; 1013 AA.
 XX
 AC AAM38678;
 XX
 DT 22-OCT-2001 (first entry)

Human polypeptide SEQ ID NO 1823.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 leukaemia.
 OS Homo sapiens.
 PN WO200153312-A1.
 XX PD 26-JUL-2001.
 XX PF 26-DEC-2000; 2000WO-US34263.
 XX PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-052317.
 PR 09-JUL-2000; 2000US-058042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-053450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0653036.
 PR 29-NOV-2000; 2000US-0727344.
 PA (HYSE-) HYSEQ INC.

XX (HYSE-) HYSEQ INC.

Example 3; SEQ ID NO 1823; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification.

Sequence 1013 AA;

Score 29; DB 22; Length 1013;

Best Local Similarity 100.0%; Pred. No. 7.2e+02; Mismatches 6; Conservative 0; Indels 0; Gaps 0;

QY 1 LEPRSS 6
Db 147 leprss 152

RESULT 11
AAM38680
ID AAM38680 standard; Protein; 1025 AA.
XX AAM38680;
AC

Query Match Score 29; DB 22; Length 1025;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02; Mismatches 6; Conservative 0; Indels 0; Gaps 0;
 QY 1 LEPRSS 6
Db 147 leprss 152

Query Match Score 29; DB 22; Length 1025;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02; Mismatches 6; Conservative 0; Indels 0; Gaps 0;
 QY 1 LEPRSS 6
Db 147 leprss 152

RESULT 12

Thu Jun 6 15:17:13 2002

us-09-627-383-1.rag

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GenCore version 4.5
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Om protein - protein search, using sw model

Run on: June 6, 2002, 13:03:48 ; Search time 12.96 Seconds
(without alignments)
11.308 Million cell updates/sec

Title: US-09-627-383-1
Perfect score: 29
Sequence: 1 LEPRA S 6
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 231628 seqs, 24425594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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4: /cgn2_6/patdata/2/iaa/6B_COMB_pep:*,
5: /cgn2_6/patdata/2/iaa/PCNTS_COMB_pep:*,
6: /cgn2_6/patdata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	29	100.0	1261 1	US-08-764-100-26
2	29	100.0	1385 2	US-08-687-390-7
3	29	100.0	2548 4	US-09-172-422-1
4	29	100.0	2887 4	US-08-462-467B-2
5	29	100.0	2887 4	US-08-462-467B-8
6	29	100.0	3218 1	US-08-764-100-27
7	26	89.7	43 2	US-08-552-816A-43
8	26	89.7	1788 2	US-08-902-284-2
9	26	89.7	7257 3	US-09-335-409-5
10	26	89.7	7257 4	US-09-568-103-5
11	26	89.7	7257 4	US-09-567-969-5
12	26	89.7	7257 4	US-09-568-480-5
13	26	89.7	7257 4	US-09-568-416-5
14	26	89.7	7257 4	US-09-568-472-5
15	25	86.2	102 2	US-08-808-982-8
16	25	86.2	102 4	US-09-902A-8
17	25	86.2	118 4	US-09-202-712-17
18	25	86.2	159 3	US-08-390-333A-5
19	25	86.2	221 3	US-08-390-333A-6
20	25	86.2	297 1	US-07-866-580-6
21	25	86.2	297 1	US-08-077-673-6
22	25	86.2	297 1	US-08-478-922-6
23	25	86.2	297 3	US-09-105-298-6
24	25	86.2	297 3	US-08-06-281A-10
25	25	86.2	297 4	US-09-097-231-10
26	25	86.2	413 3	US-08-90-353A-7
27	86.2	0	US-08-390-353A-1	

ALIGNMENTS

RESULT 1
US-08-764-100-26
; Sequence 26, Application US/08764100
; Patent No. 5773700
; GENERAL INFORMATION:
; APPLICANT: van Grinsven J., Martinus Q.
; APPLICANT: De Haan, Petrus T.
; APPLICANT: Gieloen L., Johannes J.
; APPLICANT: Peters, Birk
; APPLICANT: Goldbach, Robert W.
; TITLE OF INVENTION: Improvements in or Relating to Organic Compounds
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sandoz Agro, Inc
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,100
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 800
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,064
; FILING DATE:
; APPLICATION NUMBER: US 08/032,235
; FILING DATE: 17-MAR-1993
; APPLICATION NUMBER: GB 9206016.9
; FILING DATE: 19-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5773700-1s, Allen E.
; REGISTRATION NUMBER: 34,490
; REFERENCE/DOCKET NUMBER: 137-1061
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 354-3592
; TELEFAX: (415) 857-1125
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1261 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

US-08-764-100-26

; APPLICANT: Duhl, David

; APPLICANT: Gorman, Susan W.

; APPLICANT: Leung, Song

; APPLICANT: Sheffield, Val

; TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYPEPTIDES,

; FILE REFERENCE: 200130442

; CURRENT APPLICATION NUMBER: US/09/172,422A

; CURRENT FILING DATE: 1998-10-14

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO: 1

; LENGTH: 2548

; TYPE: PRT

; ORGANISM: Homo sapien

RESULT 2
US-08-687-399-7
Sequence 7, Application US/08687399
Patent No. 5928381

; GENERAL INFORMATION:

; APPLICANT: Toft, Annette H.

; ATTORNEY/AGENT INFORMATION:

; NAME: Marchet, Dorthe

; ADDRESS: Pedersen, Hanne H.

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/687,399

; FILING DATE:

; CLASSIFICATION: 008

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J.

; ADDRESS: Registration Number: 33,728

; REFERENCE/DOCKET NUMBER: 4127.204-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-878-9655

; TELEFAX: 212-867-0123

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1385 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-687-399-7

Query Match 100.0%; Score 29; DB 2; Length 1385;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; ATTORNEY/AGENT INFORMATION:

; NAME: Hisko, Bart S.

; REGISTRATION NUMBER: 32,572

; REFERENCE/DOCKET NUMBER: 5474R

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (513) 627-0633

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2887 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

RESULT 3
US 09-172-422-1
; Sequence 1, Application US/09172422A
; Patent No. 6300485
; GENERAL INFORMATION:
; APPLICANT: Adams, Arwen E.
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Ying
; ADDRESS: Chin, Choi YingRESULT 4
US-08-462-467B-2
Sequence 2, Application US/08462467B
Patent No. 6210999
; GENERAL INFORMATION:
; APPLICANT: Rosenbaum, Jan S
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,467B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ross, Ross
; ADDRESS: The Procter & Gamble Company
; STREET: 11810 East Miami River Road
; CITY: Ross
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-462-467B-2Query Match 100.0%; Score 29; DB 4; Length 2548;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; ATTORNEY/AGENT INFORMATION:

; NAME: Hisko, Bart S.

; REGISTRATION NUMBER: 32,572

; REFERENCE/DOCKET NUMBER: 5474R

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (513) 627-0630

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2887 amino acids

; TYPE: amino acid

; STRANDEDNESS: protein

; TOPOLOGY: protein

; US-08-462-467B-2

Query Match 100.0%; Score 29; DB 4; Length 2887;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0;
 Matches 6; Conservative 0; Indels 0; Gaps 0;

QY 1 LEPRAS 6
 Db 2034 LEPRAS 2039

RESULT 5

US-08-462-467B-8

Sequence 8, Application US/08462467B

Patient No. 6210899

GENERAL INFORMATION:

APPLICANT: Rosenbaum, Jan S

TITLE OF INVENTION: The Use of a BMP Protein Receptor

TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells

TITLE OF INVENTION: Co-Transfected With a Type II BMP Receptor

TITLE OF INVENTION: BMP Receptor

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Procter & Gamble Company

STREET: 11810 East Miami River Road

CITY: Ross

STATE: OH

ZIP: USA

COUNTRY: USA

COMPUTER READABLE FORM:

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/7764,100

FILING DATE: 06-DEC-1996

CLASSIFICATION: 800

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/214,064

FILING DATE:

APPLICATION NUMBER: US 08/032,235

FILING DATE: 17-MAR-1993

APPLICATION NUMBER: GB 9206016, 9

FILING DATE: 19-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5773700r is Allen E.

REGISTRATION NUMBER: 34,490

REFERENCE/DOCKET NUMBER: 137-1061

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 354-3592

TELEFAX: (415) 857-1125

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 3218 amino acids

TELECOMMUNICATION INFORMATION:

TELEPHONE: (513) 627-0633

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 2887 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: protein

US-08-462-467B-8

Query Match 100.0%; Score 29; DB 4; Length 2887;

Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0;

Matches 6; Conservative 0; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: van Gansven J., Martinus Q.

APPLICANT: De Haan, Petrus T.

APPLICANT: Gielen L., Johannes J.

APPLICANT: Peters, Dirk

APPLICANT: Goldbach, Robert W.

TITLE OF INVENTION: Improvements in or Relating to Organic

RESULT 6

US-08-764-100-27

Sequence 27, Application US/08764100

Patient No. 5773700

GENERAL INFORMATION:

APPLICANT: Marshall, O'Toole, Gerstein, Murray & Borun

COUNTRY: United States of America

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.25 (EPO)

TITLE OF INVENTION: Compounds
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sandoz Ago, Inc
 STREET: 975 California Avenue
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sandoz Ago, Inc
 STREET: 975 California Avenue
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Procter & Gamble Company
 STREET: 11810 East Miami River Road
 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45136

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Procter & Gamble Company
 STREET: 11810 East Miami River Road
 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45136

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Procter & Gamble Company
 STREET: 11810 East Miami River Road
 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45136

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Procter & Gamble Company
 STREET: 11810 East Miami River Road
 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45136

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Procter & Gamble Company
 STREET: 11810 East Miami River Road
 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45136

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Procter & Gamble Company
 STREET: 11810 East Miami River Road
 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45136

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Procter & Gamble Company
 STREET: 11810 East Miami River Road
 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45136

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Procter & Gamble Company
 STREET: 11810 East Miami River Road
 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45136

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Procter & Gamble Company
 STREET: 11810 East Miami River Road
 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45136

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 27

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 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45136

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/652,816A
 FILING DATE: 23-MAY-1996
 CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9125579.4
 FILING DATE: 02-DEC-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9125579.8
 FILING DATE: 02-DEC-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9206318.9
 FILING DATE: 24-MAR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9206372.6
 FILING DATE: 23-SEP-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9525004.9
 FILING DATE: 07-DEC-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9610824.6
 FILING DATE: 23-MAY-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCW/GB92/02240
 FILING DATE: 02-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/244,597
 FILING DATE: 01-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 26811/33308
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 43 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-652-816A-43

RESULT 8
 US-08-284-2
 ; Sequence 2, Application US/08962284
 ; Parent No. 5985608
 ; GENERAL INFORMATION:
 ; APPLICANT: Lura, Elizabeth J.
 ; APPLICANT: Pestonjamasp, Kersi N.
 ; APPLICANT: Pope, Robert K.
 ; APPLICANT: Wulfkuhl, Julia D.
 ; TITLE OF INVENTION: ACTIN-BINDING POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 31
 ; NUMBER OF INVENTION: AND NUCLEIC ACIDS ENCODING THE SAME
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible

Query Match 89.7%; Score 26; DB 2; Length 43;
 Best Local Similarity 83.3%; Pred. No. 29; Mismatches 1; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Missmatches 0;

QY 1 LEPRAS 6
 Db 32 LEPRAS 37

RESULT 9
 US-09-335409-5
 ; Sequence 5, Application US/09335409
 ; Patent No. 6121029
 ; GENERAL INFORMATION:
 ; APPLICANT: Schupp, Thomas
 ; APPLICANT: Ligon, James
 ; APPLICANT: Molnar, Istvan
 ; APPLICANT: Zirkle, Ross
 ; APPLICANT: Cyr, Devon
 ; APPLICANT: Goerlich, Joern
 ; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
 ; FILE REFERENCE: 4-30582A
 ; CURRENT APPLICATION NUMBER: US/09/335,409
 ; CURRENT FILING DATE: 1999-06-17
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 7257
 ; TYPE: PRT
 ; ORGANISM: Sorangium cellulosum
 US-09-335409-5

Query Match 89.7%; Score 26; DB 3; Length 7257;
 Best Local Similarity 83.3%; Pred. No. 5.4e+03; Mismatches 1; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Missmatches 0;

QY 1 LEPRAS 6
 Db 2587 LDPRAS 2592

RESULT 10
 US-09-568102-5
 ; Sequence 5, Application US/09568102
 ; Patent No. 6346404
 ; GENERAL INFORMATION:
 ; APPLICANT: Schupp, Thomas
 ; APPLICANT: Ligon, James
 ; APPLICANT: Molnar, Istvan

APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,480
; CURRENT FILING DATE: 2000-05-10
; PRIORITY APPLICATION NUMBER: 09/335,409
; PRIORITY FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-09-568-102-5

Query Match Score 26; DB 4; Length 7257;
Best Local Similarity 89.7%; Pred. No. 5.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
Db 2587 LDPRAS 2592

RESULT 11
US-09-567-969-5
; Sequence 5, Application US/09567969
; Patent No. 6355457
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567, 969
; CURRENT FILING DATE: 2000-05-10
; PRIORITY APPLICATION NUMBER: 09/335, 409
; PRIORITY FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-09-567-969-5

Query Match Score 26; DB 4; Length 7257;
Best Local Similarity 89.7%; Pred. No. 5.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
Db 2587 LDPRAS 2592

RESULT 13
US-09-568-486-5
; Sequence 5, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568, 486
; PRIORITY APPLICATION NUMBER: 09/335, 409
; PRIORITY FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-09-568-486-5

Query Match Score 26; DB 4; Length 7257;
Best Local Similarity 89.7%; Pred. No. 5.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
Db 2587 LDPRAS 2592

RESULT 14
US-09-568-472-5
; Sequence 5, Application US/09568472
; Patent No. 6358119
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568, 472

CURRENT FILING DATE: 2000-05-10
; PRIORITY APPLICATION NUMBER: 09/335,409
; PRIORITY FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-09-568-472-5

Search completed: June 6, 2002, 13:04:11
Job time: 23 sec

Query Match 89 7%; Score 26; DB 4; Length 7257;
Best Local Similarity 83 3%; Pred. No. 5.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPPAS 6
Db 2587 LDPRAS 2592

RESULT 15
US-08-808-982-8
; Sequence 8, Application US/08808982
PATENT NO. 5939271
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: Leonardo, E. David
APPLICANT: Hink, Lindsay
APPLICANT: Masu, Masayuki
APPLICANT: Kazuko, Keino-Maeu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808, 982
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCG96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-808-982-8

Query Match 86 2%; Score 25; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPPA 5
Db 13 LEPPA 17

Thu Jun 6 15:17:14 2002

us-09-627-383-1.rai

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

June 6, 2002, 13:03:48 ; Search time 15 Seconds

(without alignments)
38.436 Million cell updates/sec

Title: US-09-627-383-1

Perfect score: 29

Sequence: 1 LEPRSS 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 71;*

pir1;*

pir2;*

pir3;*

pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	29	100.0	162	2 A75529	hypothetical protein - Deinococcus radiodurans
2	29	100.0	242	2 G82642	conserved hypothetical protein
3	29	100.0	1397	2 T46554	hypothetical protein
4	29	100.0	256	2 T3099	miosin-SmGAP protein
5	27	93.1	201	2 JC5176	Junction-specific conserved hypothetical transporter
6	27	93.1	366	2 G53176	iron containing al
7	27	93.1	388	2 AG444	oxidoreductase, ir
8	27	93.1	422	2 HB2236	ribosomal protein
9	26	89.7	214	2 D75576	undecaprenyl pyrophosphate
10	26	89.7	238	2 S5009	probable DNA polymerase
11	26	89.7	254	2 AE3355	conserved hypothetical protein
12	26	89.7	321	2 F75287	hypothetical protein
13	26	89.7	352	2 G8336	conserved hypothetical protein
14	26	89.7	391	2 T38882	hypothetical protein
15	26	89.7	461	2 AH0373	cysteine--tRNA lig
16	26	89.7	465	1 F62630	cysteine--tRNA lig
17	26	89.7	465	2 D71884	cysteine--tRNA lig
18	26	89.7	477	2 T39867	hypothetical protein
19	26	89.7	561	2 S62552	hypothetical protein
20	26	89.7	562	2 A9713	hypothetical protein
21	26	89.7	601	2 T32486	hypothetical protein
22	26	89.7	609	2 G81750	conserved hypothetical protein
23	26	89.7	710	1 S71965	serine/threonine-protein kinase (EC 3.4.22)
24	26	89.7	821	1 B34482	DNA-directed RNA polymerase orf
25	26	89.7	836	2 T07222	probable guanine transposase - Escherichia coli K-12
26	26	89.7	986	2 T41809	transposase (EC 6.5.1.2)
27	26	89.7	987	2 T40411	Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrasco, D.M.; Carrer
28	26	89.7	988	2 T01477	R.; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acecio, M.; Alvarenga, R.
29	26	89.7	988	4 S58114	Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrasco, D.M.; Carrer

ALIGNMENTS

RESULT 1
A73359
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000

C;accession: A73539
R;WHITE, O.; EISEN, J.A.; HEIDELBERG, J.F.; HICKNEY, E.K.; PETERSON, J.D.; DODSON, R.J.; M.; SHEN, M.; VAMATHAVAN, J.J.; LAM, P.; McDONALD, L.; UTTERBACK, T.; ZALEWSKI, C.; S.; SMITH, H.O.; VENTER, J.C.; FRASER, C.M.
Science 286, 1571-1577, 1999
A;title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;reference number: A75250; NID:2003696
A;accession: A73539
A;status: preliminary
A; molecule type: DNA
A; residues: 1-162 <WHI>
A; cross-references: GB:AE002017; GB:AE00513; NID:96459527; PIDN:AAFL1308.1; PID:9645
A; experimental source: strain R1
C; genetics:
A; gene: DR1748
A; map position: 1
C; superfamily: Deinococcus radiodurans hypothetical protein DR1748

Query Match Score 100.0%; Score 29; DB 2; Length 162;
Best Local Similarity 100.0%; Prod. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPRSS 6
Db 151 LEPRSS 156

RESULT 2
G82642
conserved hypothetical protein XE1737 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;accession: G82642
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
A; title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; reference number: A82515; NID:2036717
A; note: For a complete list of authors see reference number A59328 below
A; accession: G82642
A; status: preliminary
A; molecule type: DNA
A; residues: 1-242 <SIM>
A; cross-references: GB:AE003997; GB:AE003849; NID:9106805; PIDN:AAF84546.1; GSPDB:GN
A; experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acecio, M.; Alvarenga, R.

as-Netto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiger chado, M.A.; Madeira, A.M.B.N.; Madeira, M.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsuoka, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Authors: da Silva, A.C.R.; da Silva, R.G.; Santelli, R.V.; Sasaki, M.; Tsuhako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovyski-Almeida, S.; Vettore, A.L.; A; Reference number: A59328
 A; Contents: annotation
 C; Genetics:
 A; Gene: XFI737

Query Match Similarity 100.0%; Score 29; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 21; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 75 LEPRAS 80

RESULT 3

T46354 hypothetical protein DKFZp434F1016.1 - human (fragment)

C;Species: Homo sapiens (man)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
 C;Accession: T46354
 C;Author: Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 C;Submitted to the Protein Sequence Database, January 2000
 A;Reference number: Z23037
 A;Accession: T46354
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1397 <AAA>
 A;Cross-references: EMBL:AL137287
 A;Experimental source: adult testis; clone DKFZp434F1016
 C;Genetics:
 C;Note: DKFZp434F1016.1
 C;Superfamily: protein kinase C zinc-binding repeat homology <KZN>
 F;849-897/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match Similarity 100.0%; Score 29; DB 2; Length 1397;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 1206 LEPRAS 1211

RESULT 4

T31099 myosin-RhGAP protein, Myr 7 - rat

C;Species: Rattus norvegicus (Norway rat)
 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 08-Sep-2000
 C;Accession: T31099
 R;Chieregatti, E.; Gaertner, A.; Stoessl, H.E.; Baehler, M.
 A;Description: Myr 7 is a novel myosin-Rho-GAP molecule expressed in rat brain.
 A;Reference number: 220982
 A;Accession: T31099
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2626 <CH1>
 A;Cross-references: EMBL:AJ001713; NID:e1357083; PID:e1357084; PLDN:CAA04946.1
 A;Experimental source: strain Sprague-Dawley
 C;Genetics:
 A;Gene: myoga

Query Match Similarity 93.1%; Score 27; DB 2; Length 201;
 Best Local Similarity 83.3%; Pred. No. 53; Mismatches 1; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 146 MEPRAS 151

RESULT 6

G95376 conserved hypothetical protein SMA1676 [imported] - Sinorhizobium meliloti (strain 10 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C;Accession: G95376
 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barlow-Hubler, F.; B; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli

C;Superfamily: protein kinase C zinc-binding repeat homology; myosin motor domain hom P;145-1005/Domain: myosin motor domain homology #status atypical <MM>
 F;2068-2116/Domain: protein kinase C zinc-binding repeat homology <K2N>

Query Match Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 2443 LEPRAS 2448

RESULT 5

JC5476 junction-specific DNA-binding protein ruvA - Pseudomonas aeruginosa
 N;Alternate names: Holliday junction DNA helicase RuVA
 C;Species: Pseudomonas aeruginosa
 C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 31-Dec-2000
 C;Accession: JC5476; H8324
 R;Hishida, T.; Iwazaki, H.; Ishioka, K.; Shinagawa, H.
 A;Title: Molecular analysis of the Pseudomonas aeruginosa genes, ruvA, ruvB and ruvC,
 A;Reference number: JC5476; M00D:97136691
 A;Accession: JC5476
 A;Molecule type: DNA
 A;Residues: 1-201 <KIS>
 A;Cross-references: DDBJ:D83138; NID:91183837; PIDN:BAA11818.1; PID:91183841
 A;Experimental source: strain PA01
 A;Note: the authors translated the initiation codon GNG for residue 1 as Met
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Kiesey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A;Reference number: A82950; M00D:20437337
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-201 <STO>
 A;Cross-references: GB:AE004530; GB:AE004091; NID:99946865; PIDN:AAG04355.1; GSDB:GN
 A;Experimental source: strain PA01
 A;Gene: ruvA; PA0966
 A;Function:
 A;Description: acting as specificity factor that targets ruvB protein; ruvA protein a
 ate stages of homologous genetic recombination and DNA repair
 C;Superfamily: Holliday junction DNA helicase ruva
 C;Keywords: DNA binding; DNA recombination; DNA repair
 F;106-126/Domain: Helix-hairpin-helix #status predicted <HHH>

A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Accession: G95376
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-366 <KUR>
A; Cross-references: GB:AE006469; PIDN:AAK65577.1; PID:914524057; GSPDB:GN0165
A; Experimental source: strain 101, megaplasmid PSymA
R; Gaibert, F.; Flan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barley-Hubler, P.;
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Fedderspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lealaure,
hebault, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A86039; MUID:21368234; PMID:11474104
A; Contents: annotation
A; Gene: Sma1676
A; Genome: plasmid

Query Match 93.1%; Score 27; DB 2; Length 366;
Best Local Similarity 83.3%; Pred. No. 1e-02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LEPRAS 6
Db 292 IEPGRAS 297

RESULT 7
RG3444 transporter BMEI1541 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AG3444
R;Delvecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Muier, C.; Los, T.; Ivanova,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3444
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52722.1; PID:917983551; GSPDB:GN0190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1541
A;Map Position: I

Query Match 93.1%; Score 27; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LEPRAS 6
Db 236 MEBRAS 241

RESULT 8
HB2236 iron containing alcohol dehydrogenase VC1147 [imported] - Vibrio cholerae (strain N16961)
C;Species: Vibrio cholerae
C;Accession: HB2236 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: HB2236
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
L.R.R.; Metlano, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: AD2035; MUID:206833

Query Match 93.1%; Score 27; DB 2; Length 422;
Best Local Similarity 83.3%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LEPRAS 6
Db 396 IEPGRAS 401

RESULT 9
D75576 oxidoreductase, iron-sulfur subunit - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: D75576
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.M.;
S.; Smith, H.O.; Ventre, J.C.; Fricker, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:2036896
A;Accession: D75576
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <WHI>
A;Cross-references: GB:AB001863; GB:AE001825; NID:96460670; PIDN:AAF12402.1; PID:96460670
A;Experimental source: Strain R1
A;Genetics:
C;Genetics:
A;Gene: DRA0235
A;Map Position: 2
C;Superfamily: isoquinoline 1-oxidoreductase alpha chain; ferredoxin [2Fe-2S] homolog
F;68,73,76,88/Binding site: 2Fe-2S cluster (Gys) (covalent) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 214;
Best Local Similarity 83.3%; Pred. No. 9.9; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LEPRAS 6
Db 45 LDPRAS 50

RESULT 10
S50809 ribosomal protein L17, mitochondrial - yeast (Saccharomyces cerevisiae)
N;Alternate names: HRD238 protein; mitochondrial ribosomal protein Yml8; protein J112
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 08-Sep-1995 #text_change 13-Aug-1999
C;Accession: S50809; S47128; S14890; S19235; S56837
R;Vandenberg, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
Year: 11, 57-60, 1995
A;Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae
A;Reference number: S50798; MUID:95282514
A;Accession: S50809
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-238 <PAN>
A;Cross-references: EMBL:Z34288; NID:9498992; PIDN:CAAR4060.1; PID:9499004
A;Contents: annotation

R; Vanderbult, M.; Durand, P.; Blon, C.; Portetelle, D.; Hilger, F.
 R; submitted to the EMBL data Library, June 1994
 A; Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae.
 A; Reference number: S47117
 A; Accession: S47117
 A; Molecule type: DNA
 A; Residues: 1-238 <VAV>
 R; Kitakawa, M.; Grothmann, L.; Graack, H.R.; Isono, K.
 Nucleic Acids Res. 18, 1521-1529, 1990
 A; Title: Cloning and characterization of nuclear genes for two mitochondrial ribosomal RNA genes in *Saccharomyces cerevisiae*
 A; Reference number: S14889; MUID:90221879
 A; Accession: S14890
 A; Molecule type: DNA
 A; Residues: 1-81, 'G', 83-238 <KIT>
 A; Cross-references: EMBL:X53841; NID:93981; PIDN:CAA37834.1; PID:93982
 A; Accession: S19235
 A; Molecular type: Protein
 A; Residues: 2-28 <KIT2>
 A; Experimental source: strain DC5, YNN27
 R; Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
 submitted to the Protein Sequence Database, September 1995
 A; Accession: S56837
 A; Molecule type: DNA
 A; Residues: 1-238 <POH>
 A; Cross-references: EMBL:249338; NID:91008210; PIDN:CAA89354.1; PID:91008211; MIPS:YJL063c
 A; Genetics:
 A; Gene: SGD:MRPL8
 A; Cross-references: SGD:S0003599; MIPS:YJL063c
 A; Map position: 10L
 A; Genome: nuclear
 C; Superfamily: Escherichia coli ribosomal protein L17
 C; Keywords: mitochondrial; protein biosynthesis; ribosome
 F; 2-238/Product: ribosomal protein L17 #status experimental <MAT>

Query Match 89.7%; Score 26; DB 2; Length 238;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy	1	LEPRAS	6
	:		
Db	111	LEPRAN	116

RESULT 11

A83355 undecaprenyl pyrophosphate synthetase (EC 2.5.1.31) [imported] - *Brucella melitensis* (strain 13/94)
 C; Species: *Brucella melitensis*
 C; Accession: AB3355
 C; Deinococcus, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltskaya, E.; Selkov, E.; Elzer, P.H.; Hagiwara, S.; O'Callaghan, D.; Letesson, J.C.; The genome sequence of the facultative intracellular pathogen *Brucella melitensis* B1/94: reference number: AD3252; PMID:11756698
 A; Accession: AB3355
 A; Molecule type: DNA
 A; Residues: 1-254 <KUR>
 A; Experimental source: strain 13/94
 C; Genetics:
 A; Map position: I
 C; Superfamily: conserved hypothetical protein YBR002c
 C; Keywords: transferrase

```

RESULT    12
F75287
Probable DNA polymerase III subunit - Deinococcus radiurans (strain Rl)
C;Species: Deinococcus radiurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: F75287
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioreistant bacterium Deinococcus radiurans Rl.
A;Reference number: A75250; MUID:20036895
A;Accession: F75287
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-321 <NNI>
A;Cross-references: GB:AE002064; GB:AE000513; NID:96460134; PIDN:AFF11878.1; PID:9646
A;Experimental source: strain Rl
C;Genetics:
A;Gene: D2332
A;Map position: 1

Query Match          89 %;   Score 26;   DB 2;   Length 321;
Best Local Similarity 83.3%; Pred. No. 1.5e+02; 0;  Mismatches
Matches      5;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;
Qy          1 LEPRAS 6
Db          86 LEPRAT 91

RESULT    13
G83636
conserved hypothetical protein PA0069 [imported] - Pseudomonas aeruginosa (strain PAO
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83636
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; i
admin, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
., Lory, S.; Olson, M.V.
Nature 406, 950-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: G83636
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <STO>
A;Cross-references: GB:AE00446; GB:AE004091; NID:99945886; PIDN:AAG03459.1; GSPPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0069

Query Match          89 %;   Score 26;   DB 2;   Length 352;
Best Local Similarity 83.3%; Pred. No. 1.7e+02; 0;  Mismatches
Matches      5;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;
Qy          1 LEPRAS 6
Db          200 LEPRAA 205

RESULT    14
T388B2
hypothetical protein SPAC4H3.02c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe

```

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
 C;Accession: T3882
 R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, February 1996
 A;Reference number: 221807
 A;Accession: T3882
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-391 <MUR>
 A;Cross-references: EMBL:Z69380; PIDN:CAA93341.1; GSPDB:GN00066; SPDB:SPAC4H3.02c
 A;Experimental source: strain 972h-; cosmid c4H3
 C;Genetics:
 A;Gene: SPDB:SPAC4H3.02c
 A;Map position: 1
 A;Map position: 56/2
 C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4H3.02c

Query Match 89.7% Score 26; DB 2; Length 391;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LEPRAS 6
 Db 37 LQPRAS 42

RESULT 15
 A|0373 cysteine--tRNA ligase (EC 6.1.1.16) [imported] - Yersinia pestis (strain CO92),
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
 C;Accession: A|0373
 R;Parthill, J.; Wien, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarrada, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 -A;Accession: A|0373
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-461 <KIR>
 A;Cross-references: GB:AL590842; PIDN:CAC92315.1; PID:g15981026; GSPDB:GN00175
 C;Genetics:
 A;Gene: cysS
 C;Superfamily: cysteine--tRNA ligase
 C;Keywords: liase

Query Match 89.7% Score 26; DB 2; Length 461;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LEPRAS 6
 Db 110 LEPRAT 115

Search completed: June 6, 2002, 13:04:33
 Job time: 45 sec

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GenCore version 4.5
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OM protein - protein search, using SW model.
 Run on: June 6, 2002, 13:04:38 ; Search time 10.31 Seconds

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Maximum Match 0%
 Listing first 45 summaries

Title: US-09-627-383-1
 Perfect score: 29
 Sequence: 1 LEPRAS 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
 Listing first 45 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	29	100.0	1026	TAC2_HUMAN
2	27	93.1	201	1 RUVA_PSEAE
3	26	89.7	238	1 RMO8_YEAST
4	26	89.7	335	1 B3G5_CRIGR
5	26	89.7	335	1 B3G3_HUMAN
6	26	89.7	335	1 B3G3_MOUSE
7	26	89.7	391	1 TAY_SCHPO
8	26	89.7	465	1 SYC_HELP
9	26	89.7	465	1 TAI7_SCHPO
10	26	89.7	561	1 ALUL_HUMAN
11	26	89.7	591	1 PKN6_MYXAA
12	26	89.7	710	1 CANJ_RAT
13	26	89.7	821	1 RPQC_CHLVO
14	26	89.7	836	1 PEX6_RAT
15	26	89.7	978	1 DPOL_NPVB
16	26	89.7	986	1 TNP9_ECOLI
17	26	89.7	988	1 SC16_YEAST
18	26	89.7	2194	1 IRL_CAEEL
19	26	89.7	4753	1 DSR6_HUMAN
20	25	86.2	190	1 DSR5_HUMAN
21	25	86.2	287	1 UL24_ITIVY
22	25	86.2	295	1 ACTR_BOVIN
23	25	86.2	297	1 SGK_RAT
24	25	86.2	300	1 MOVP_AMVVA
25	25	86.2	300	1 MOVP_AVMPA
26	25	86.2	300	1 MOVP_AVMPA
27	25	86.2	300	1 MOVP_AMVVA
28	25	86.2	309	1 NUSC_STRG8
29	25	86.2	430	1 SGK_RAT
30	25	86.2	431	1 SGK_MOUSE
31	25	86.2	431	1 SGK_RABIT
32	25	86.2	452	1 SGK_RABIT
33	25	86.2	452	1 F26 YEAST

ALIGNMENTS

RESULT 1
 TAC2_HUMAN STANDARD: PRT: 1026 AA.
 ID TAC2_HUMAN DT 16-OCT-2001 (Rel. 40, Last sequence update)
 AC 095359; 09N25; Q9W41; DE Transforming acidic coiled-coil-containing protein 2 (Anti zuai-1)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE (AZU-1).
 RA TAC22.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=fetal brain, Brain, and Skeletal muscle;
 RX MEDLINE-20570083; PubMed-11121038;
 RA Gergely F., Karlsson C., Still I.H., Cowell J.K., Kilmartin J.,
 RA Raff J.W.;
 RA "The TACC domain identifies a family of centrosomal proteins that can interact with microtubules.",
 RT PROCE. NATL. ACADE. SCI. U.S.A. 97:14352-14357(2000).
 RL [2]
 RA SEQUENCE OF 375-1026 FROM N.A. (ISOFORM 2).
 RX MEDLINE-20214826; PubMed=10749935;
 RA Chev H.-M., Schmeichel K.L., Mian I.S., Lelievre S., Petersen O.W.,
 RA Bisselli M.J.;
 RA "AUJ1: a candidate breast tumor suppressor and biomarker for tumor progression."
 RT Mol. Biol. Cell 11:1357-1367(2000);
 RL [3]
 RA SEQUENCE OF 44-1026 FROM N.A. (ISOFORM 3).
 RA PU J., Li C., Rodriguez M., Banerjee D.;
 RA "Expression of TACC2 protein mRNA in human microvascular endothelial cells."
 RT Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 RL -- FUNCTION: MAY PLAY A ROLE IN ORGANIZING CENTROSOMAL MICROTUBULES.
 CC MAY ACT AS A TUMOR SUPPRESSOR PROTEIN. MAY REPRESENT A TUMOR PROGRESSION MARKER.
 CC -- SUBUNIT: INTERACTS WITH MICROTUBULES.
 CC -- SUBCELLULAR LOCATION: NUCLEAR; CONCENTRATED AT CENTROSOMES.
 CC -- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
 CC -- SIMILARITY: BELONGS TO THE TACC FAMILY.
 CC

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EMBL

EMBL: AF095791; AAC64968.2; -

EMBL: AF176646; AAC63433.1; ALT_INIT.

DR InterPro; IPR00456; Ribosomal_L17.
 DR Pfam; PF01196; Ribosomal_L17; 1.
 DR PRODOM; PDO04277; Ribosomal_L17; 1.
 DR PROSITE; PS01167; Ribosomal_L17; 1.
 KW Ribosomal protein; Mitochondrion.
 FT CONFLICT 82 D -> G (IN REF. 1).
 SQ SEQUENCE 238 AA; 26945 MW; A130EFD95E8719BA CRC64;
 Query Match 89.7%; Score 26; DB 1; Length 238;
 Best Local Similarity 83.3%; Pred. No. 51; Mismatches 5; Conservative 1; MisMatches 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 Db 111 LEPRAN 116

RESULT 4
 B3G3_CRIGR STANDARD; PRT; 335 AA.
 AC Q9WU47;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 01-MAR-2002 (Rel. 41; Last annotation update)
 DE Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3
 DE (EC 2.4.-1,3)-glucuronosyltransferase-I (GICAT-I) (UDP-GlCUA:Gal Beta-1,3-Gal-R
 DE glucuronosyltransferase) (GICAT-I).
 OS Cricetus cricetus (Chinese hamster).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus
 OX NCBI_TAXID=10029;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=99175158; PubMed=10075678;
 RA Wei G., Bai X., Sarkar A.K., Esko J.D.;
 RT "Formation of HNK-1 determinants and the glycosaminoglycan
 tetrasaccharide linkage region by UDP-GlCUA:Galactose beta-1,3-
 glucoosyltransferases.",
 RT J. Biol. Chem. 274:7857-7864 (1999).
 CC FUNCTION: GLYCOSAMINOGLYCAN BIOSYNTHESIS. INVOLVED IN FORMING THE
 CC LINKAGE TETRASACCHARIDE PRESENT IN HEPARAN SULFATE AND CHONDROITIN
 CC SULFATE. TRANSFERS A GLUCURONIC ACID MOIETY FROM THE URIDINE
 CC DIPHOSPHATE-GLUCURONIC ACID (UDP-GlCUA) TO THE COMMON LINKAGE
 CC REGION TRISACCHARIDE GAL BETA 1-4GAL BETA 1-4XYL COVALENTLY BOUND
 CC TO A SER RESIDUE AT THE GLYCOSAMINOGLYCAN ATTACHMENT SITE OF
 CC PROTEOGLYCANS. CAN ALSO PLAY A ROLE IN THE BIOSYNTHESIS OF L2/HNK-
 CC 1 CARBOHYDRATE EPITOPE ON GLYCOPROTEINS. HIGHEST ACTIVITY SEEN
 CC WITH GAL-BETA-1,3-GAL-BETA-O-R (WHERE R=NAPHTHALENEMETHANOL OR
 CC BENZYL ALCOHOL).
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + 3-beta-D-galactosyl-4-
 CC beta-D-galactosyl-O-beta-D-xylosylprotein = UDP + 3-beta-D-
 CC xylosylprotein.
 CC -!- COFACTOR: MANGANESE.
 CC -!- PATHWAY: GLYCOSAMINE.
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE II membrane protein. Golgi.
 CC -!- TISSUE SPECIFICITY: LIVER, BRAIN AND HEART. MODERATE EXPRESSION
 CC SEEN IN LUNG, SKELETAL MUSCLE, KIDNEY AND TESTIS.
 CC -!- PTM: N-GLYCOSYLATED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 43.
 CC
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 CC or send an email to license@isb-sib.ch).

RESULT 5
 B3G3_HUMAN STANDARD; PRT; 335 AA.
 AC Q94766; Q9UBP0;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 01-MAR-2002 (Rel. 41; Last annotation update)
 DE Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3
 DE (EC 2.4.-1,3)-glucuronosyltransferase-I (Beta-1,3-glucuronosyltransferase 3)
 DE (Glucuronosyltransferase-I) (GICAT-I) (UDP-GlCUA:Gal beta-1,3-Gal-R
 DE glucuronosyltransferase) (GICAT-I).
 RN [1] SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RP TISSUE=Placenta;
 RX MEDLINE=98175919; PubMed=9506957;
 RA Kitagawa H., Tone Y., Tamura J.-I., Neumann K.W., Ogawa T., Oka S.,
 RA Kawasaki T., Sugahara K.;
 RT "Molecular cloning and expression of glucuronosyltransferase I involved
 RT in the biosynthesis of the glycosaminoglycan-protein linkage region of
 RT proteoglycans.",
 RT J. Biol. Chem. 273:6615-6618 (1998).
 RN [2] SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS.
 RX MEDLINE=2042846; PubMed=10842173;
 RA Ouzzine M., Gilberti S., Netter P., Magdalou J., Fournel-Gigleux S.,
 RT "Structure/function of the human Galbeta1,3-glucuronosyltransferase.
 RT Bimolecular and functional activity are mediated by two crucial
 RT cysteine residues";
 RT J. Biol. Chem. 275:28254-28260 (2000).
 RN [3] SEQUENCE OF 9-335 FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=99128347; PubMed=9927678;
 RA Herman T., Horvitz H.R.;
 RT "Three proteins involved in Caenorhabditis elegans vulval invagination
 RT are similar to components of a glycosylation pathway.",
 RT Proc. Natl. Acad. Sci. U.S.A. 96:974-979 (1999).
 RL [4] CHARACTERIZATION.
 RP MEDLINE=99456856; PubMed=10526176;
 RX Tone Y., Kitagawa H., Imiya K., Oka S., Kawasaki T., Sugahara K.;
 RA "One Kir4/Kir5.1 heteromeric channel is a glycosaminoglycan-protein linkage
 RT involved in the biosynthesis of the glycosaminoglycan-protein linkage

RESULT 7
 VAY2-SCHPO STANDARD; PRT; 391 AA.
 ID YAY2-SCHPO
 AC Q10210;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Hypothetical 44.7 kDa protein C4H3_02C in chromosome I.
 GN SPACH3_02C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OX NCBI_TAXID=4896;
 RN SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Murphy L., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Z69380; CAA93411.1; -;
 DR HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 391 AA; 44716 MW; 72D8F088B15E50A8 CRC64;

RESULT 8
 Query Match 89.7%; Score 26; DB 1; Length 391;
 Best Local Similarity 83.3%; Pred. No. 87;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 AC SYC_HELPJ STANDARD; PRT; 465 AA.
 ID SYC_HELPJ
 AC 09ZKWC;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine-tRNA ligase)
 GN CYSS OR JHP0818.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923582;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
 RA Smith D.R., Noonan B., Guild B.L., de Jonge B.L., Carmel G.,
 RA Tummolo P.J., Caruso A., Urias-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180 (1999).
 CC -1- CATALYTIC ACTIVITY: AMP + L-cysteine + tRNA(CYS) = AMP +
 CC diphosphate + L-cysteinyl-tRNA(CYS).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

RESULT 9
 Query Match 89.7%; Score 26; DB 1; Length 465;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 AC SYC_HELPY STANDARD; PRT; 465 AA.
 ID SYC_HELPY
 AC P41259;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine-tRNA ligase)
 DE (CYSS).
 GN CYSS OR HP0886.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9739467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J.J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Goedeyne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
 RA "The complete genome sequence of the gastric pathogen Helicobacter
 pylori.";
 RL Nature 388:539-547 (1997).
 RN [2]
 RP SEQUENCE OF 278-465 FROM N.A.
 RC STRAIN=ATCC 49503 / 60190;
 RX MEDLINE=94193753; PubMed=8144644;
 RA Cover T.L., Tummuru M.R., Cao P., Thompson S.A., Blaser M.J.;
 RT "Divergence of genetic sequences for the vacuolating cytotoxin among
 Helicobacter pylori strains";
 RL J. Biol. Chem. 269:10566-10573 (1994).
 RN [3]
 RP SEQUENCE OF 407-465 FROM N.A.

RC STRAIN=CCUG 17874 / NCTC 11638;
 RX MEDLINE=9422514; PubMed=8168917;
 RA Phadnis S.H., Liver D.J., Janzon L., Normark S., Westblom T.U.;
 RT "Pathological significance and molecular characterization of the
 vacuolating toxin gene of Helicobacter pylori.";
 RL Infect. Immun. 62:1557-1565(1994).
 CC -1 CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = AMP +
 CC diphosphate + L-cysteinyl-tRNA(Cys).
 CC -1 SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1 SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.
 CC STRONG, TO METHIONYL-tRNA SYNTHETASE.

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CC -----

CC AE000598; AAD07934; 1; -.
 DR EMBL; U05676; AAA18866; 1; -.
 DR EMBL; U07145; AAA18866; 1; -.
 DR PIR; C53739; C53739.
 DR PIR886; -.
 DR InterPro; IPR02308; tRNA-synt_le.
 DR InterPro; IPR00412; tRNA-synt_i.
 DR Pfam; PF01406; tRNA-synt_1e; 1.
 DR PRINTS; PR00583; TRNASTRNHCYS.
 DR PROSITE; PS00178; R_A-TRNA_LIGASE_I; FALSE NEG.
 DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 29 39 "HIGH" REGION.
 FT SITE 269 273 "KMSKS" REGION.
 FT BINDING 272 272 ATP (BY SIMILARITY).
 FT VARIANT 280 280 V -> I (IN STRAIN ATCC 49503).
 FT VARIANT 332 332 T -> N (IN STRAIN ATCC 49503).
 FT VARIANT 392 392 I -> V (IN STRAIN ATCC 49503).
 FT VARIANT 432 432 R -> Q (IN STRAINS ATCC 49503 AND NCTC
 11638).
 FT VARIANT 434 434 D -> N (IN STRAIN NCTC 11638).
 FT VARIANT 440 440 S -> H (IN STRAIN ATCC 49503).
 SQ SEQUENCE 465 AA; 53131 MN; B7053D58BCD8/F30 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 465;
 Best Local Similarity 83.3%; Pred. No. 1.e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LEPRAS 6
 Db 109 LEPKAS 114

RESULT 10

YALI_SCHPO STANDARD; PRT; 561 AA.

YALI_SCHPO STANDARD; PRT; 561 AA.

AC Q09847;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

ID YALI_SCHPO STANDARD; PRT; 561 AA.

DE Hypothetical 62.5 kDa protein C24B11.07C in chromosome I.

GN SPAC24B11.07C.

OS Schizosaccharomyces pombe (Fission Yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetidales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

NCBI_TAXID=4896;

[1]

SEQUENCE FROM N.A.

SPRAIN972;

Odell C., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;

RL Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

RX -1 SIMILARITY: TO S.POME SPCC1902.02.

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CC -----

DR EMBL; Z67757; CAA91772; 1; -.
 DR HYPOTHETICAL PROTEIN;
 SQ SEQUENCE 561 AA; 62463 MW; 146D40D7CF42A096 CRC64;

Qy	1 LEPRAS 6	Db	527 VEPRAS 532

Query Match 89.7%; Score 26; DB 1; Length 561;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

ALU1_HUMAN STANDARD; PRT; 591 AA.

ALU1_HUMAN STANDARD; PRT; 591 AA.

AC P39188;

DT 01-FEB-1995 (Rel. 31, created)
 DT 01-FEB-1995 (Rel. 31, last sequence update)

DE Alu subfamily J sequence contamination warning entry.

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TAXID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95021758; PubMed=7935834;

RX Claverie J.-M., Makalowski W.;

RX "Alu alert";

RT Nature 371:752-752(1994).
 RL [2]

RP CONCEPT.

RX MEDLINE=92241891; PubMed=1572661;

RA Claverie J.-M.;

RT "Identifying coding exons by similarity search: alu-derived and other
 RT potentially misleading protein sequences.",
 RT Genomics 12:838-841(1992).

RN [3]

RP ALU FAMILIES CLASSIFICATION

RX MEDLINE=883333009; PubMed=3138422;

RA Quentin Y.;

RT "The Alu family developed through successive waves of fixation
 RT closely connected with primate lineage history.",
 RT J. Mol. Evol. 27:194-202(1988).

RN [4]

RP ALU FAMILIES CLASSIFICATION

RX MEDLINE=91178815; PubMed=1706781;

RA Jurka J., Milosavljevic A.;
 RA Jurka J., Milosavljevic A.;

RT "Reconstruction and analysis of human Alu genes.",
 RT J. Mol. Evol. 32:1105-121(1991).

RL "RECONSTRUCTION AND ANALYSIS OF THE HUMAN ALU GENOME",
 CC J. Mol. Evol. 32:1105-121(1991).

CC -1 MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
 CC THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
 CC CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
 CC FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
 CC REPEATS.

CC -1 MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
 CC CODON. 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.

CC -1 CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
 CC POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
 CC ACID SEQUENCES.

CC -!- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL T1T. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CC CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS CC LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES. CC BEING REPORTED.

CC -!- CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE CC CODING NUCLEOTIDE SEQUENCE.

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CC DR EMBL; U40656; AAB40050.1.; -.

CC DR HSSP; P00523; 2PTK.

CC DR InterPro; IPR00719; Euk_Pkinase.

CC DR InterPro; IPR02290; Ser_thr_Pkinase.

CC DR PRAM; PF00059; Pkinase_1.

CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.

CC DR PROSITE; PS00111; PROTEIN_KINASE_DOM_1.

CC KW BINDING; serine/threonine-protein kinase; ATP-binding; transmembrane; Phosphorylation; Repeat.

CC FT DOMAIN 1 482 CYTOPLASMIC (POTENTIAL).

CC FT TRANSMEM 483 503 POTENTIAL, PERIPHERAL, (POTENTIAL).

CC FT DOMAIN 504 710 PROTEIN KINASE.

CC FT NP_BIND 6 280 ATP (BY SIMILARITY).

CC FT BINDING 12 20 ATP (BY SIMILARITY).

CC FT ACT_SITE 38 38 ATP (BY SIMILARITY).

CC FT DOMAIN 143 143 BY SIMILARITY.

CC FT TRANSMEM 337 369 2 X 12 AA REPEAT OF P-V/A-D-S-T-S-P-T-

CC FT REPEAT 337 348 P-M-P.

CC FT REPEAT 358 369 1.

CC FT REPEAT 358 369 2.

CC SQ SEQUENCE 710 AA; 74621 MW; EDCF670072DCBAA CRC64;

Query Match 89.7%; Score 26; DB 1; Length 591; Best Local Similarity 83.3%; Pred. No. 1.4e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPRSS 6 ||||:|

Db 22 LEPRSS 27

RESULT 12

PKN6_MYXHA ID PRN6_MYXHA STANDARD: PRT; 710 AA.

AC P54738; DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Serine/threonine-protein kinase pkn6 (EC 2.7.1. -).

GN PKN6.

OS Myxococcus xanthus.

Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxoccaceae; Myxococcus.

OC NCBITaxID=34;

RN [1]

RP SEQUENCE FROM N.A.

RT STRAIN=DZEL;

RA MEDLINE=96310380; PubMed=8733241;

RA Zhang W., Inouye M., Inouye S.;

RT "Reciprocal regulation of the differentiation of Myxococcus xanthus by Pkn5 and Pkn6, eukaryotic-like Ser/Thr protein kinases.", Mol. Microbiol. 20:435-447 (1996).

-!- FUNCTION: PRN6 AND PKN6 MAY HAVE RECIPROCAL ROLES IN GROWTH AND DEVELOPMENT. PKN6 MAY BE A TRANSMEMBRANE SENSOR OF EXTERNAL SIGNALS FOR DEVELOPMENT.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY THROUGHOUT THE LIFE

CC CYCLE, WITH SLIGHT INCREASES AT AN EARLY STAGE OF DEVELOPMENT.

CC -!- PTM: AUTOPHOSPHORYLATED AT SERINE AND THREONINE RESIDUES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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CC or send an email to license@isb-sib.ch).

CC DR EMBL; U40656; AAB40050.1.; -.

CC DR HSSP; P00523; 2PTK.

CC DR InterPro; IPR00719; Euk_Pkinase.

CC DR InterPro; IPR02290; Ser_thr_Pkinase.

CC DR PRAM; PF00059; Pkinase_1.

CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.

CC DR PROSITE; PS00111; PROTEIN_KINASE_DOM_1.

CC KW BINDING; serine/threonine-protein kinase; ATP-binding; transmembrane; Phosphorylation; Repeat.

CC FT DOMAIN 1 482 CYTOPLASMIC (POTENTIAL).

CC FT TRANSMEM 483 503 POTENTIAL, PERIPHERAL, (POTENTIAL).

CC FT DOMAIN 504 710 PROTEIN KINASE.

CC FT NP_BIND 6 280 ATP (BY SIMILARITY).

CC FT BINDING 12 20 ATP (BY SIMILARITY).

CC FT ACT_SITE 38 38 ATP (BY SIMILARITY).

CC FT DOMAIN 143 143 BY SIMILARITY.

CC FT TRANSMEM 337 369 2 X 12 AA REPEAT OF P-V/A-D-S-T-S-P-T-

CC FT REPEAT 337 348 P-M-P.

CC FT REPEAT 358 369 1.

CC FT REPEAT 358 369 2.

CC SQ SEQUENCE 710 AA; 74621 MW; EDCF670072DCBAA CRC64;

Query Match 89.7%; Score 26; DB 1; Length 710; Best Local Similarity 83.3%; Pred. No. 1.7e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPRSS 6 ||||:|

Db 379 LEPRSS 384

RESULT 13

CAN3_RAT ID CAN3_RAT STANDARD: PRT; 821 AA.

AC P16259; DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calpain 3 large subunit (EC 3.4.22.17) (Calpain L3) (Calpain p94', large [catalytic] subunit) (Calcium-activated neutral protease 3) (CANP 3) (muscle-specific calcium-activated neutral protease 3 large subunit).

DE CAPN3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Rutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBITaxID=10116;

RP SEQUENCE FROM N.A.

RC TISSUE-Skeletal muscle;

RA MEDLINE=90062125; PubMed=2555341;

RA Sorimachi H., ImaJoh Ohmi S., Emori Y., Kawasaki H., Ohno S., Minami Y., Suzuki K.;

RA "Molecular cloning of a novel mammalian calcium-dependent protease distinct from both m- and mu-types. Specific expression of the mRNA in skeletal muscle.", J. Biol. Chem. 264:20106-20111(1989); J. Biol. Chem. 264:20106-20111(1989);

CC -!- FUNCTION: Calcium-regulated non lysosomal thiol-protease.

CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-| -xaa, Met-| -xaa or

-!- ARG-L-Xaa with Leu or Val as the P2 residue.
 ENZYME REGULATION: Activated by micromolar concentrations of calcium and inhibited by calpestatin.
 SUBUNIT: Heterodimer of a large (catalytic) and a small (regulatory) subunit.
 SUBCELLULAR LOCATION: Cytoplasmic.
 TISSUE SPECIFICITY: SKELETAL MUSCLE.
 -!- MISCELLANEOUS: IN RAT THERE SEEMS TO BE 2 TYPES OF CALPAIN:
 UBIQUITOUS FORMS - CALPAIN I (MICROMOLEES CA++ REQUIRING) AND
 CALPAIN II (MILLI-MOLE CA++ REQUIRING), AND TISSUE SPECIFIC FORMS -
 CALPAIN PI4 AND NCII, THE SMALL UNIT IS COMMON TO ALL FORMS.
 -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
 -!- SIMILARITY: BELONGS TO PEPTIDE FAMILY C2; ALSO KNOWN AS THE CALPAIN FAMILY OF THIOL PROTEASES.

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 EMBL: J05121; AAA41790.1; -.
 PIR: B34488; B34488.
 DR HSPB; P04532; 1DKV.
 DR MEROPS; C02.004; -.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR01300; Peptidase_C2.
 DR InterPro; IPR00169; Thiolprot_act-site.
 DR Pfam: PF01067; Calpain_III; 1.
 DR Pfam; PF00365; Efhand; 3.
 DR Pfam; PF00648; Peptidase_C2; 1.
 DR PRINTS; PR00704; CALPATN.
 DR SMART; SNO0230; CUSPC; 1.
 DR SMART; SNO0054; EFN; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00640; THIOL_PROTEASE ASN; FALSE_NEG.
 KW Hydrolase; Thiol protease; Calcium-binding; Multigene family; Repeat.
 DOMAIN 49 234 THIOL PROTEASE ASN; FALSE_NEG.
 DOMAIN 49 234 THIOL PROTEASE ASN; FALSE_NEG.
 FT DOMAIN 235 428 THIOL PROTEASE ASN; FALSE_NEG.
 FT DOMAIN 429 585 THIOL PROTEASE ASN; FALSE_NEG.
 FT DOMAIN 587 649 THIOL PROTEASE ASN; FALSE_NEG.
 FT DOMAIN 650 820 THIOL PROTEASE ASN; FALSE_NEG.
 FT CA_BIND 735 746 THIOL PROTEASE ASN; FALSE_NEG.
 FT DOMAIN 800 781 THIOL PROTEASE ASN; FALSE_NEG.
 FT ACT_SITE 129 129 THIOL PROTEASE ASN; FALSE_NEG.
 FT ACT_SITE 334 334 THIOL PROTEASE ASN; FALSE_NEG.
 FT ACT_SITE 358 358 THIOL PROTEASE ASN; FALSE_NEG.
 SEQUENCE 821 AA; 94127 MW; 27EAEAD2FEA19FBF CRC64;

 Query Match 89.7%; Score 26; DB 1; Length 836;
 Best Local Similarity 83.3%; Pred No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 Db 188 LEPRSS 193

 RESULT 15
 PEX6_RAT
 ID PEX6_RAT
 AC P54777; O55097; STANDARD; PRT; 978 AA.
 DT 01-Oct-1996 (Rel. 34, Created)
 DT 01-Oct-1996 (Rel. 34, Last sequence update)
 DT 16-Oct-2001 (Rel. 40, Last annotation update)
 DE Peroxisome assembly factor-2 (PAF-2) (peroxisomal-type ATPase 1)
 DE (Peroxin-6).
 GN PEX6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RP [1] SEQUENCE FROM N.A.
 RC STRAIN=FISCHER 344; TISSUE=Liver;
 RX MEDLINE=96083986; PubMed=7493019;
 RA Tsukamoto T., Miura S., Nakai T., Yokota S., Shimozawa N.,
 RA Suzuki Y., Orii T., Fujiki Y., Sakai F., Bogaki A., Yasuno H.,
 RA Osumi T.;
 RT Peroxisome assembly factor-2, a putative ATPase cloned by functional

RT complementation on a peroxisome-deficient mammalian cell mutant.";
 RL Nat. Genet. 11:395-401(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Tsukamoto T.; Hashiguchi N.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 CC -I- FUNCTION: INVOLVED IN PEROXISOME BIOSYNTHESIS. REQUIRED FOR
 CC STABILITY OF THE PTS1 RECEPTOR.
 CC -I- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN, PEROXISOME.
 CC -I- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
 CC
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 CC
 DR EMBL; D63673; BAA05824; 1. -.
 DR EMBL; D89660; BAA24931; 1.
 DR EMBL; D89657; BAA24931; 1; JOINED.
 DR EMBL; D89658; BAA24931; 1; JOINED.
 DR EMBL; D89659; BAA24931; 1; JOINED.
 DR InterPro; IPR003593; AAA.
 DR InterPro; IPR003960; AAA_sub.
 DR InterPro; IPR003959; AAA_subam.
 DR Pfam; PF00004; AAA; 2.
 DR SMARV; SM00382; AAA; 1.
 DR PROSITE; PS00574; AAA; 1.
 KW Peroxisome; ATP-binding; Repeat.
 FT NP_BIND 470 477 ATP (POTENTIAL).
 FT NP_BIND 742 749 ATP (POTENTIAL).
 FT MUTAGEN 476 476 K->A: NO LOSS OF FUNCTION.
 FT MUTAGEN 748 748 K->A: LOSS OF FUNCTION.
 FT CONFLICT 299 299 D -> G (IN REF. 2).
 FT CONFLICT 333 333 V -> A (IN REF. 2).
 FT CONFLICT 343 343 Q -> R (IN REF. 2).
 FT CONFLICT 546 546 R -> C (IN REF. 2).
 SQ SEQUENCE 978 AA; 104426 MW; F72319B7E95EA97 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 978;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPRAS 6
 Db 935 LEPRSS 940

Search completed: June 6, 2002, 13:08:09
 Job time: 211 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 6, 2002, 13:04:13 ; search time 25.04 Seconds

(without alignments)
41.452 Million cell updates/sec

Title: US-09-627-383-1

Perfect score: 29

Sequence: 1 LEPRAS 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL_19:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_micr:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rabbit:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description	RESULT	1
1	29	100.0	162	16 Q9RTL2	ID Q9RTL2	PRELIMINARY; PRT; 162 AA.
2	29	100.0	242	16 Q9PCP1	AC Q9RTL2;	
3	29	100.0	526	4 Q9NUY2	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
4	29	100.0	594	10 Q9LGZ7	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
5	29	100.0	635	5 Q24564	DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
6	29	100.0	1060	5 Q46055	DE HYPOTHETICAL 17.0 KDA PROTEIN.	
7	29	100.0	1077	5 Q9V8HB	GN DR1748.	
8	29	100.0	1397	4 Q9NTG2	OS Deinococcus radiodurans.	
9	29	100.0	2359	11 Q9E6Q0	OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.	
10	29	100.0	2548	4 Q9UNJ2	OX NCBI_TAXID-1299;	
11	29	100.0	2616	11 Q9ZIN3	RN [1]	
12	27	93.1	311	2 Q68976	RP SEQUENCE FROM N.A.	
13	27	93.1	356	16 Q986C9	RC STRAIN=R1;	
14	27	93.1	357	7 Q95560	RX MEDLINE=20036896; PubMed=10567266;	
15	27	93.1	357	7 Q95410	RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Grinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pampille W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski R.A., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleschmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., RA Fraser C.M.;	
16	27	93.1	357	7 Q95411	RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";	
17	27	93.1	366	16 Q92YG1	RT Science 286:1715-1777(1999).	
18	27	93.1	385	16 Q92KK9	DR EMBL; AE003016; AAF11308.1; -.	
19	27	93.1	422	16 Q9KSV9	DR ITGR; DR148; -.	
20	27	93.1	887	16 Q98EH3	KW HYPOTHETICAL protein; Complete Proteome.	
21	26	89.7	104	4 Q9P0E3	SEQUENCE 162 AA; 16986 MW; 3023A49A17A7BF4 CRC64;	
22	26	89.7	147	11 Q925S3	QY 1 LEPRAS 6	
23	26	89.7	153	2 Q4626	Db 151 LEPRAS 156	
24	26	89.7	170	11 Q925S2		
25	26	89.7	174	16 Q989Y3		
26	26	89.7	177	16 Q92t87		
27	26	89.7	214	16 Q9RY3		
28	26	89.7	252	3 Q9ff62		
29	26	89.7	279	16 Q984S7		
30	26	89.7	321	16 Q9RZ7		
31	26	89.7	335	4 Q9KE7		
32	26	89.7	339	10 Q9C9M7		
33	26	89.7	348	10 Q9C9M7		
34	26	89.7	352	10 Q94GZ7		
35	26	89.7	352	16 Q91763		
36	26	89.7	360	2 Q9FA57		
37	26	89.7	366	2 Q96106		
38	26	89.7	407	4 Q9ILW0		
39	26	89.7	477	3 Q92968		
40	26	89.7	479	4 Q9WZ16		
41	26	89.7	481	11 Q99PF2		
42	26	89.7	493	11 Q9R113		
43	26	89.7	547	5 Q9W637		
44	26	89.7	562	10 Q9S713		
45	26	89.7	601	5 Q17402		
					ALIGMENTS	

RESULT	2	OX NCBI_TaxID=9606;
Q9PCP1	PRELIMINARY;	RN [1]
Q9PCP1	PRT; 242 AA.	RP SEQUENCE FROM N.A.
ID Q9PCP1:		RC TISSUE=PLACENTA;
DT 01-OCT-2000 (TREMBLREL. 15, Created)		RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsumura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)		RT "NECD human cDNA sequencing Project.";
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)		RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DE HYPOTHETICAL PROTEIN XP1737.		GN XPF1737.
OS Xylella fastidiosa.		DR EMBL: AK001933; BAA91979.1; -.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; Xylella.		DR HSSP; Q07960; IGP.
OC NCBITAXID=2371;		DR InterPro; IPR001018; RhoGAP.
RN [1]		DR SMART; SW00324; RhoGAP; 1.
RP SEQUENCE FROM N.A.		SQ SEQUENCE 526 AA; 59212 MW; 868624871E4C860C CRC64;
RC STRAIN=945C;		
RX MEDLINE=20365717; PubMed=10910347;		
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Aceñolo M., Alvaenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barrios M.H., Bonacorsi E.D., Bordón S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carrasco D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena A., El-Dorry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., França S.C., Franco M.C., Frohne M., Furian L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Jungueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., Lemos E.G.M., Lemos M.V., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madiira A.M.B.N., Madeira H.M.F., Marinho C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miracco C., Miyaki C.Y., Monteiro-Vitalelo C.B., Moon D.H., Nagai M.A., Nascenteiro A.L.T.O., Netto L.E.S., Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Oliveira M.C., de Oliveira R.C., Palmeiro D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., Rosa V.E., Jr., de Sa R.G., Santelli R.V., Swasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzio M.F., Truffi D., Tsuhako M.H., Vailada H., Van Sluys M.A., Verjovskij-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.; RT "The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> ."; RL Nature 406:151-155(2000). DR EMBL; AP003997; AAF84461; -; DR Hypothetical protein; Complete proteome; SEQUENCE 242 AA; 25385 MW; 857F70152F2B0C1B CRC64;		
Query Match 100.0%; Score 29; DB 16; Length 242;		
Best Local Similarity 100.0%; Pred. No. 43; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 1 LEPRAS 6		
Db 75 LEPRAS 80		
RESULT 3		
Q9NY2 PRELIMINARY; PRT; 526 AA.		
AC Q9NY2;		
DT 01-OCT-2000 (TREMBLREL. 15, Created)		
DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)		
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)		
DE CONA FLJ11061 FIS, CLONE PLACE1004777, WEAKLY SIMILAR TO N-CHIMARRIN.		
OS Homo sapiens (Human).		
OC Erikarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.		
RESULT 5		
Q24564 PRELIMINARY; PRT; 635 AA.		
ID Q24564; Q24564; Q24564; Q24564; Q24564;		
AC Q24564; Q24564; Q24564; Q24564; Q24564;		
DT 01-NOV-1996 (TREMBLREL. 01, Created)		
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)		
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)		
DE MER PROTEIN (CYTOSKELETON PROTEIN).		
DE MER OR EMBR2 OR DMLRIN OR CG14228.		
GN OS Drosophil melanogaster (Fruit fly).		
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Drosophilidae; Drosophila.		

QY	1 LEPRAS 6
RP	
RN	SEQUENCE FROM N.A.
RC	STRAIN-BERKELEY;
RX	MEDLINE=20196005; PubMed=10731132;
RA	Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortsman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter G., Helt G., Nelson C.R., Miklos G.L.G., Baldwin J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Brookstein P., Brottier P., Borikova D., Botchan M.R., Bouck J., Brokstein P., Cadieu E., Chandra I., Burttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew T., Dietz S.M., Dodson K., Doup L.E., Downes M., Duan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabril A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Jaihali M., Kalush F., Karpen G.H., Ke Z., Kenmison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei J., Levitsky A.R., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Mekelburg G., Mishina N.V., Molarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reiner B.C., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue C.K., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.-A., Ye J.-H., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of <i>Drosophila melanogaster</i> ."; Science 287:2183-2195(2000).; [2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96334672; PubMed=86666699;
RA	McCartney B.M., Fehon R.G.,
RT	"Distinct cellular and subcellular patterns of expression imply the neurofibromatosis 2 tumor suppressor, merlin.";
RT	functions for the <i>Drosophila</i> homologues of moesin and the J. Cell Biol. 133:843-852(1996).; [3]
RP	SEQUENCE OF 218-307 FROM N.A.
RA	Wing P., Fleming J.T., Gobel V., Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
DR	EMBL: AE003512; AAF49005.1; -.
DR	EMBL: U23799; AA65050.1; -.
DR	EMBL: U23799; AA65050.1; -.
DR	FlyBase; FlyBase ID: FBgn000299; Band 4.1.
DR	InterPro; IPR000798; Ezrin-radixin-moesin.
DR	Pfam; PF00373; Band 4.1; 1.
DR	Prints; PRO0935; BAND41.
DR	SMART; SM00295; B41; 1.
DR	PROSITE; PS50057; BAND41_3; 1.
SO	SEQUENCE; 635 AA; 74492 MW; 940D6B8A00160A3F CRC64;
Query Match	100%; Score 29; DB 5; Length 635;
Best Local Similarity	100.0%; Pred. No. 1.1e+02;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT	6
ID	04055
AC	046055;
DT	01-JUN-1998 (TREMBREL 06, Created)
DT	01-NOV-1999 (TREMBREL 12, Last sequence update)
DT	01-JUN-2001 (TREMBREL 17, Last annotation update)
DE	EG165H7.3 PROTEIN.
GN	L1)1BB OR EG:165H7.3 OR CG3923.
OS	<i>Drosophila melanogaster</i> (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyoidea; Drosophilidae; Drosophila.
OX	NCBI_TAXID=227;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	de Pablo B., Madueno E., Modolell J.;
RL	"Sequencing the distal X chromosome of <i>Drosophila melanogaster</i> ."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Benos P.;
RL	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AL009188; CAA15674.2; -.
DR	FlyBase; FBgn0001337; 1(1)BB.
DR	InterPro; IPR001494; IBN_NT.
SQ	SEQUENCE: 1060 AA; 119276 MW; 650B03CD25DB9156 CRC64;
Query Match	100%; Score 29; DB 5; Length 1060;
Best Local Similarity	100.0%; Pred. No. 1.9e+02;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 LEPRAS 6
DR	5 LEPRAS 10
RESULT	7
ID	0918HB
AC	0918HB
DT	01-MAY-2000 (TREMBREL 13, Created)
DT	01-MAY-2000 (TREMBREL 13, Last sequence update)
DT	01-MAY-2000 (TREMBREL 13, Last annotation update)
DE	CG12263 PROTEIN.
GN	CG12263.
OS	<i>Drosophila melanogaster</i> (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyoidea; Drosophilidae; Drosophila.
OC	NCBI_TAXID=227;
RP	SEQUENCE FROM N.A.
RC	STRAIN-BERKELEY;
RX	MEDLINE=20196005; PubMed=10731132;
RA	Adams M.D., Celinkier S.E., Holt R.A., Evans C.A., Gocayne J.D., Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortsman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bayraktaroglu L., Beasley P.S., Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Cadieu E., Chandra I., Burgis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L., Davis P., Davies P.,

DR	InterPro; IPR000048; IQ.
DR	InterPro; IPR001609; myosin_head.
DR	InterPro; IPR000159; RA.
DR	InterPro; IPR000198; RhogAP.
DR	Pfam; PF00130; DAG_Pe-bind; 1.
DR	Pfam; PF00612; IQ; 5.
DR	Pfam; PF00063; myosin_head; 2.
DR	Pfam; PF00788; RA; 1.
DR	Pfam; PF00620; RhogAP; 1.
DR	PRINTS; PRO0193; MYOSINHEAVY.
DR	PRODOM; PD000355; myosin_head; 2.
DR	SMART; SM00109; C1; 1.
DR	SMART; SM00015; IQ; 5.
DR	SMART; SM00242; MSC; 1.
DR	SMART; SM00314; RA; 1.
DR	SMART; SM00324; RhogAP; 1.
DR	PROSITE; PS00419; DAG_Pe_BIND_DOM_1; UNKNOWN_1.
DR	PROSITE; PS50096; IQ; 1.
DR	SEQUENCE; 2548 AA; 292703 MW; B93B76C2A0E9A356 CRC64;
Qy	1 LEPRAS 6
Db	2357 LEPRAS 2362
RESULT 11	
ID	Q9Z1N3 PRELIMINARY; PRT; 2626 AA.
AC	Q9Z1N3; 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	MYOSIN-RHOGAP PROTEIN MYR 7.
GN	MYO9A
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RP	[1] SEQUENCE FROM N.A.
RA	Chieragatti E., Gaertner A., Stoeffler H.E., Baehler M.; "Myr 7 is a novel myosin-Rho-GAP molecule expressed in rat brain.", Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RT	Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RL	EMBL; AJ001713; CAA04946.1; -.
DR	HSSP; IMND; AA_tRNA_ligase_II.
DR	InterPro; IPR002106; AA_tRNA_ligase_II.
DR	InterPro; IPR002219; DAG_Pe-bind.
DR	InterPro; IPR00048; IQ.
DR	InterPro; IPR001609; myosin_head.
DR	InterPro; IPR00159; RA.
DR	InterPro; IPR000198; RhogAP.
DR	Pfam; PF00130; DAG_Pe-bind; 1.
DR	Pfam; PF00612; IQ; 5.
DR	Pfam; PF00063; myosin_head; 2.
DR	Pfam; PF00788; RA; 1.
DR	Pfam; PF00620; RhogAP; 1.
DR	PRINTS; PRO0193; MYOSINHEAVY.
DR	PRODOM; PD000355; myosin_head; 2.
DR	SMART; SM00105; IQ; 5.
DR	SMART; SM00242; MSC; 1.
DR	SMART; SM00314; RA; 1.
DR	SMART; SM00324; RhogAP; 1.
DR	PROSITE; PS00179; AA_TRNA_LIGASE_II_1; UNKNOWN_1.
DR	PROSITE; PS00479; DAG_Pe_BIND_DOM_1; UNKNOWN_1.
DR	PROSITE; PS50081; DAG_Pe_BIND_DOM_2; 2.
SQ	SEQUENCE; 2626 AA; 301378 MW; 3F70610271ED791 CRC64;
Query Match Best Local Similarity 100.0%; Score 29; DB 4; Length 2548; Matches 6; Conservative 6; Predicted No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;	
Matches 6; Conservative 6; Predicted No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 LEPRAS 6
Db	2443 LEPRAS 2448
RESULT 12	
ID	Q9Z1N6 PRELIMINARY; PRT; 311 AA.
AC	Q9Z1N6; 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	HYPOTHETICAL 35.1 KDA PROTEIN (FRAGMENT).
OS	Bacillus meilensis.
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Brucella.
OX	NCBI_TaxID=29459;
RP	[1] SEQUENCE FROM N.A.
RC	STRAIN=133;
RA	Hernandez-Castro R., Sahagun-Ruiz A., Verdugo-Rodriguez A., Suarez-Guemes F.; Waghela S., Gutierrez-Pabello A.J., Adams A.G., Suarez-Guemes F.;
RT	"Cloning and sequence of hypothetical protein of <i>Brucella melitensis</i> ". Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RL	Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF059568; AAC14571.1; -.
DR	InterPro; IPR002787; DUF85.
DR	Prints; PF01932; DUF85; 1.
DR	ProDom; PD011382; DUF85; 1.
KW	Hypothetical protein.
FT	NON_TER 1
SEQUENCE 311 AA; 35078 MW; B523B28790C7DAB6 CRC64;	
Query Match Best Local Similarity 93.1%; Score 27; DB 2; Length 311; Matches 5; Conservative 5; Predicted No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;	
Matches 5; Conservative 5; Predicted No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 LEPRAS 6
Db	173 MPRAS 178
RESULT 13	
ID	Q986C9 Q986C9 PRELIMINARY; PRT; 356 AA.
AC	Q986C9; 01-OCT-2001 (TREMBLrel. 18, Created)
DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE	MIL7417 PROTEIN.
GN	MIL7417.
OS	Rhizobium loti (<i>Mesorhizobium loti</i>).
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Mesorhizobium.
OX	NCBI_TaxID=381;
RP	[1] SEQUENCE FROM N.A.
RA	SISTRAIN=MAFF03099;
RC	SISTRAIN=MAFF03099;
RX	MEDLINE=21082930; Pubmed=11214968;
RA	Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S., Watanabe A., Idezawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyosawa C., Kohara M., Matsunoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT	"Complete genome structure of the nitrogen-fixing symbiotic bacterium <i>Mesorhizobium loti</i> ";

Query Match 93.1%; Score 27; DB 7; Length 357;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPRAS 6
 :|||||
 Db 66 MEPRAS 71

RESULT 14

ID	PRELIMINARY;	PRT;	357 AA.
Q95560			
AC	Q95560;		
DT	01-FEB-1997 (TREMBREL. 02, Created)		
DT	01-FEB-1997 (TREMBREL. 02, Last sequence update)		
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)		
DE	MHC CLASS I (FRAGMENT).		
DR	EMBL: APO03011; BAP5324.1; - .		
DR	InterPro: IPR002787; DUF85.		
DR	Pfam: PF01932; DUF5; 1.		
DR	Prodom: PD011382; DUF85; 1.		
KW	Complete proteome.		
SQ	SEQUENCE 356 AA; 40498 MW; F7437E1708E175A4 CRC64;		
RP	SEQUENCE FROM N.A.		
RX	Medline=22218057; PubMed=1560209;		
RA	Chen Z.W., McAdam S.N., Hughes A.L., Dogon A.L., Letvin N.L., Watkins D.I.;		
RT	"Molecular cloning of orangutan and gibbon MHC class I cDNA. The HLA-A and -B loci diverged over 30 million years ago.";		
RT	J. Immunol. 148:2547-2554 (1992).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Chen Z.W., McAdam S.N., Hughes A.L., Watkins D.I.;		
RL	Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.		
CC	-1 - FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).		
CC	-1 - SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).		
DR	EMBL: US0089; AAB05072.1; - .		
DR	HSSP; 019673, HS8B		
DR	InterPro: IPR003597; Ig_C1.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR01039; MHC_I.		
DR	Pfam: PF00047; Ig; 1.		
DR	Pfam: PF00129; MHC_I; 1.		
DR	Prodom: PD000050; MHC_I; 1.		
DR	SMART: SM00407; IgI; 1.		
DR	PROSITE: PS00290; Ig_MHC; 1.		
KW	Glycoprotein; Transmembrane.		
FT	NON_TER		
SQ	SEQUENCE 357 AA; 40026 MW; 682DDFB8EDB9F361 CRC64;		

Query Match 93.1%; Score 27; DB 7; Length 357;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPRAS 6
 :|||||
 Db 61 MEPRAS 66

Search completed: June 6, 2002, 13:07:53
 Job time: 220 sec

RESULT 15

ID	PRELIMINARY;	PRT;	357 AA.
Q95410			
AC	Q95410;		
DT	01-FEB-1997 (TREMBREL. 02, Created)		
DT	01-FEB-1997 (TREMBREL. 02, Last sequence update)		

Thu Jun 6 15:17:18 2002

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